

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: April 9, 2003, 16:41:41 ; Search time 11 Seconds
(without alignments)
128,200 Million cell updates/sec

Sequence: 1 SVSEIQLMNLGKILNSMERVWLKQLQDVHNF 34
US-09-843-221a-16
P375757

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

1 number of hits satisfying chosen parameters: 6866

Minimum DB seq length: 0
Maximum DB seq length: 70

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	21.8	70	PF2L_PLAAPP	P07765 plasmodium
2	37	20.7	52	YOAH_HABIN	P56507 haemophilus
3	37	20.7	61	Y081_ARCFU	O30153 archaeoglob
4	36.5	20.4	54	XX13_XENLA	P40850 xenopus lae
5	36.5	20.4	59	SECE_BACLI	P38381 bacillus lae
6	35	19.6	60	SENN_BACNA	P21666 bacillus su
7	35	19.6	65	SENS_BACSU	P21344 bacillus su
8	34.5	19.3	27	T4C_PASTE	Q27176 paramecium
9	34.5	19.3	61	RL37_SULSO	Q97491 sulfobus
10	34.5	19.3	65	YNOL_RHIFR	P33214 rhizobium f
11	34.5	19.3	69	YFXX_AZOCA	P26486 azorhizobiu
12	33.5	18.7	29	GLUC_CHIBR	P31297 chinchilla
13	33.5	18.7	60	HM09_CABEL	P56407 caenorhabdi
14	33	18.4	30	PCG3_PACGO	P82416 pachycondyl
15	33	18.4	36	RL7_COXBU	O87502 coxiella bu
16	33	18.4	63	R24E_AERPE	Q99247 aeropyrum p
17	33	18.4	68	NTRC_AZOCA	Q04848 azorhizobiu
18	32.5	18.2	50	RL39_SCHPO	P05767 pachyosacch
19	32	17.9	29	PCG4_PACGO	P82417 pachycondyl
20	32	17.9	59	Y423_METJA	Q57866 methanococc
21	32	17.9	62	PETL_PINTH	P52805 pinus thum
22	31	17.3	52	RL32_CVACA	O19894 cyanidium c
23	31	17.3	55	Y279_RICPR	Q92498 rickettsia
24	31	17.3	66	RL35_DEIRA	Q9raw6 deinococcus
25	31	17.3	68	RL29_ARCFU	O28361 archaeoglob
26	31	17.3	70	ATFJ_RAT	P29419 rattus norv
27	30.5	17.0	26	CT21_LITCI	P81847 littoria cit
28	30.5	17.0	62	RL19_NAIZE	Q08066 zea mays (m
29	30.5	17.0	64	SECE_BACHD	Q9kge8 bacillus ha
30	30	16.8	26	MEL_APIDO	P01502 apis dorsat
31	30	16.8	30	PC25_AKGLB	P82144 agkistodon
32	30	16.8	42	YC70_WHEAT	Q9xpe5 triticum ae
33	30	16.8	44	SL1B_SHEEP	P07217 ovis aries

34	30	16.8	50	1	Y896_TREPA	O83866 treponema p
35	30	16.8	52	1	AHPD_MYCSM	Q50441 mycobacteri
36	30	16.8	58	1	SINI_BACLI	P27755 bacillus li
37	30	16.8	70	1	V43_BPT7	P03784 bacterioph
38	29.5	16.5	48	1	DPSD_AZQVI	Q44558 azotobacter
39	29	16.2	33	1	OREX_BOVIN	P56717 bos taurus
40	29	16.2	42	1	SLT_ENTCL	P39433 enterobacte
41	29	16.2	50	1	R35A_ARATH	P51422 arabidopsis
42	29	16.2	50	1	RL39_ARCFU	O28122 archaeoglob
43	29	16.2	51	1	RL39_PYRAB	Q9uy18 pyrococcus
44	29	16.2	52	1	RL39_METJA	P54056 methanococc
45	29	16.2	52	1	RPC3_BBP22	P14110 bacterioph

ALIGNMENTS

RESULT 1

PF2L_PLAAPP STANDARD; PRT; 70 AA.
AC P07765;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE PPF2L antigen (Fragment).
OS Plasmodium falciparum (isolate Palo Alto / Uganda).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=57270;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85242037; PubMed=2409532;
RA Langley G., Scherf A., Mercereau-Puijalon O., Koenen M., Kahane B.,
RA Mattei D., Guillothe M., Sibilli L., Garner I., Mueller-Hill B.,
RA Pereira da Silva L.;
RT "Characterisation of P. falciparum antigenic determinants isolated
RT from a genomic expression library by differential antibody
RT screening";
RL Nucleic Acids Res. 13:4191-4202(1985).
CC -!- MISCELLANEOUS: THIS ANTIGEN IS EXPRESSED IN ALL ERYTHROCYTIC
CC FORMS.

RESULT 2

YOAH_HABIN STANDARD; PRT; 52 AA.
ID YOAH_HABIN
AC P56507; O86238;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein H1434.2.
GN H1434.2.

Query Match

Best Local Similarity 39.1%; Score 39; DB 1; Length 70;

Mismatches 9; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Query

5 IQLMNLGKILNSMERVWLK 27

10 IYILNNIKNLKENVDLNKR 32

```
OS Haemophilus influenzae
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Usterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.D., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RD ";
RT Science 269:496-512(1995).
[2]
RP IDENTIFICATION.
RX MEDLINE=98248213; PubMed=9588799;
RA Rudd K.E., Humphrey-Smith I., Wasinger V.C., Bairoch A.;
RT "Low molecular weight proteins: a challenge for post-genomic
RT research.";
RL Electrophoresis 19:536-544(1998).
CC -1- SIMILARITY: BELONGS TO THE UPF0181 FAMILY.
CC -----
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CC -----
DR EMBL; U32822; AAC23083.1; ALT_INIT.
DR TIGR; H11434.2; -.
DR InterPro; IPR005371; UPF0181.
DR Pfam; PF03701; UPF0181.1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 52 AA; 5903 MW; FF8E364E185FB262 CRC64;
Query Match 20.7%; Score 37; DB 1; Length 52;
Best Local Similarity 22.2%; Pred. No. 1.9e+02;
Matches 6; Conservative 11; Mismatches 10; Indels 0; Gaps 0;
6 QLMNGLKHLNSMERVEWLRKKLQDVH 32
Db 17 QIQELMAQGISGGEAIQIVAKALREIH 43
RESULT 3
Y083_ARCFU
ID Y083_ARCFU STANDARD; PRT; 61 AA.
AC O30153;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein AF0083.
GN AF0083.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Klenk H.-P., Clayton R.A., Tomb J.-P., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Usterback T.,
Cotton M.D., Spriggs T., Artach P., Kaine B.P., Sykes S.M.,
Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus.";
RL Nature 390:364-370(1997).
CC -----
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CC -----
DR EMBL; AE001100; AAB91149.1; -.
DR TIGR; AF0083; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 61 AA; 7053 MW; 4096E1B2A28E7D36 CRC64;
Query Match 20.7%; Score 37; DB 1; Length 61;
Best Local Similarity 46.2%; Pred. No. 2.3e+02;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 2 VSEIQLMNGLKGH 14
Db 21 ISKPLHMQTKH 33
RESULT 4
SX13_XENLA
ID SX13_XENLA STANDARD; PRT; 54 AA.
AC P40650;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE SOX-13 protein (Fragment).
GN SOX-13.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92310993; PubMed=1614875;
RA Denny P., Swift S., Brand N., Dabhadre N., Barton P., Ashworth A.;
RT "A conserved family of genes related to the testis determining gene,
RT SRV.";
RL Nucleic Acids Res. 20:2887-2887(1992).
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -1- SIMILARITY: CONTAINS 1 HMG BOX.
CC -----
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CC -----
DR EMBL; X65656; CAA46607.1; -.
DR PIR; S21491; S21491.
DR HSSP; P48436; 189M.
DR InterPro; IPR000910; HMG_12_box.
DR Pfam; PF00505; HMG_box; 1.
DR SMART; SM00398; HMG; 1.
KW DNA-binding; Nuclear protein.
```

OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX	NCBI_TaxID=86029;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=90063530; PubMed=3269394;
RA	Wong S.-L., Wang L.-F., Doi R.H.;
RT	"Cloning and nucleotide sequence of senN, a novel 'Bacillus natto' (B. subtilis) gene that regulates expression of extracellular protein genes."
RL	J. Gen. Microbiol. 134:3269-3276(1988).
CC	- FUNCTION: REGULATES THE EXPRESSION OF EXTRACELLULAR-PROTEIN GENES OF BACILLUS NATTO.
CC	- SIMILARITY: TO SEVERAL B.SUBTILIS RNA POLYMERASE SIGMA FACTORS.
CC	- SIMILARITY: TO B.SUBTILIS SENS.
DR	PIR; A34945; A34945.
KW	Transcription regulation; DNA-binding.
FT	DNA BIND 11 31 H-T-H MOTIF (BY SIMILARITY).
SQ	SEQUENCE 60 AA; 7220 MW; OCE30106C06286P6 CRC64;
Query Match	19.6%; Score 35; DB 1; Length 60;
Best Local Similarity	27.6%; Pred. No. 4e+02;
Matches	8; Conservative 8; Mismatches 13; Indels 0; Gaps
OY	4 ETQLMHNLGKHLNSMERVWLKKLDQDVH 32
DB	26 ELLIEKNREIINSAEIMEEIYNKIDEKH 54
RESULT 7	
SENS_BACSU	STANDARD; PRT; 65 AA.
ID	SENS_BACSU STANDARD; PRT; 65 AA.
AC	P21344;
DT	01-MAY-1991 (Rel. 18, Created)
DT	01-MAY-1991 (Rel. 18, Last sequence update)
DT	15-JUN-2002 (Rel. 41, Last annotation update)
DE	Transcriptional regulatory protein sens.
GN	SENS.
OS	Bacillus subtilis.
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX	NCBI_TaxID=1423;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=9020712; PubMed=2108127;
RA	Wang L.-F., Doi R.H.;
RT	"Complex character of sens, a novel gene regulating expression of extracellular-protein genes of Bacillus subtilis.";
RL	J. Bacteriol. 172:1939-1947(1990).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN=168;
RX	MEDLINE=97346037; PubMed=9202460;
RA	Cummings N.J., Connerton I.F.;
RT	"The Bacillus subtilis 168 chromosome from sspE to kataA.";
RL	Microbiology 143:1855-1859(1997).
RN	[3]
RP	SEQUENCE FROM N.A.
RC	STRAIN=168;
RX	MEDLINE=98044033; PubMed=9384377;
RA	Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borcherst S., Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell J.B., Capuno V., Carter N.M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D., Fritz C., Fujita Y., Fuma S., Galizzi A., Galleron N., Ghim S.Y., Glaser P., Goffeau A., Golightly B.J., Grandi G., Guiseppi G., Guy B.J., Haga K., Haech J., Harwood C.R., Henaut A., Hilbert H., Holsappel S., Hosono S., Hulio M.F., Itaya M., Jones L., Joris B., Katamata D., Kasahara Y., Klaer-Blanchard M., Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M., Kurita K., Lapidus A., Lardinolis S., Lauber J., Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,

RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudesa B., Park S.H.,
 RA Farro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone P.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Seiror P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tanakoshi A., Tanaka T., Terpetra P., Tognoni A.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzneger T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.P., Zumstein E., Yoshikawa H., Danchin A.,
 RA "The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*,"
 RT Nature 390:249-256 (1997).
 RL Nature 390:249-256 (1997).
 CC -!- FUNCTION: REGULATES THE EXPRESSION OF EXTRACELLULAR-PROTEIN GENES
 CC OF *BACILLUS SUBTILIS*.
 CC -!- SIMILARITY: TO SEVERAL B. SUBTILIS RNA POLYMERASE SIGMA FACTORS.
 CC -!- SIMILARITY: TO B.NATTO SENN.
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 DR EMBL; M34826; AAA22750.1; -;
 DR EMBL; Z82044; CAB04806.1; -;
 DR EMBL; Z99108; CAB12709.1; ALT_INIT.
 DR PIR; A35150; A35150.
 DR Subtilisin; BGI0747; sens.
 KW Transcription regulation; DNA-binding; Complete proteome.
 FT DNA BIND 11 31 H-T-H MOTIF (BY SIMILARITY).
 SQ SEQUENCE 65 AA; 7912 MW; 4A685B04179CE318 CRC64;
 Query Match 19.6%; Score 35; DB 1; Length 65;
 Best Local Similarity 27.6%; Pred. No. 4.4e+02;
 Matches 8; Conservative 8; Mismatches 13; Indels 0; Gaps 0;
 QY 4 EIQLMNGLKHLNSMERVWLRKQLQDVH 32
 DB 26 ELLIKRNKEIINSALMEIYMKIDEXH 54
 P<0.001
 PART 8
 T4C PARTE STANDARD; PRT; 27 AA.
 AC Q27176;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Trichocyst matrix protein T4-C (Secretory granule protein T4-C)
 DE (T4P 4-C) (Fragment).
 GN T4C.
 OS Paramecium tetraurelia.
 OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
 OC Paramecium.
 OX NCBI_TaxID=5889;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D4-2;
 RX MEDLINE=96059477; PubMed=7579685;
 RA Madeddu L., Gautier M.-C., Vayssie L., Houari A., Sperling L.;
 RT "A large multigene family codes for the polypeptides of the
 RL crystalline trichocyst matrix in *Paramecium*,"
 RL Mol. Biol. Cell 6:649-659 (1995).
 RP PARTIAL SEQUENCE.
 RC STRAIN=D4-2;
 RX MEDLINE=95119139; PubMed=7819344;

RA Madeddu L., Gautier M.-C., le Caer J.P., de Loubresse N., Sperling L.;
 RT "Protein processing and morphogenesis of secretory granules in
 RL *Paramecium*,"
 RL Biochimie 76:329-335 (1994).
 CC -!- FUNCTION: STRUCTURAL PROTEIN THAT CRYSTALLIZE INSIDE THE
 CC TRICHO CYST MATRIX.
 CC -!- SUBCELLULAR LOCATION: TRICHO CYST. THESE ARE ARCHITECTURALLY
 CC COMPLEX SECRETORY STORAGE GRANULES-DOCKED AT THE PLASMA MEMBRANE,
 CC READY TO RAPIDLY RESPOND TO AN EXOCYTOTIC STIMULUS.
 CC -!- SIMILARITY: BELONGS TO THE TMP FAMILY.
 CC -!- DATABASE: NAME-Protein Spotlight;
 CC NOTE=Issue 3 of October 2000;
 CC WWW="http://www.expasy.org/spotlight/articles/sptlt003.html".
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 CC
 DR EMBL; U27514; AAA92614.1; -;
 KW Polyprotein; Structural protein; Multigene family.
 FT NON_TER 1 1
 FT NON_TER 27 27
 SQ SEQUENCE 27 AA; 2837 MW; 731046E30185A542 CRC64;
 Query Match 19.3%; Score 34.5; DB 1; Length 27;
 Best Local Similarity 38.1%; Pred. No. 2.1e+02;
 Matches 8; Conservative 6; Mismatches 6; Indels 1; Gaps 1;
 QY 1 SVSEIQ-LMHNGLKHLNSMER 20
 DB 2 AVGEIQILNNIASQLNGDQX 22
 RESULT 9
 RL37_SULSO STANDARD; PRT; 61 AA.
 ID RL37_SULSO
 AC Q972Q1;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 50S ribosomal protein L37e.
 GN RPL37E OR SSO6453.
 OS Sulfolobus solfataricus.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 OX NCBI_TaxID=2287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 35092 / DSM 1617 / P2;
 RX MEDLINE=21332296; PubMed=11427726;
 RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
 RA Aweez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
 RA De Moors A., Brauso G., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
 RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Theriault C., Tolstrup N.,
 RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
 RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
 RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
 RA "The complete genome of the crenarchaeon *Sulfolobus solfataricus* P2,"
 RT Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840 (2001).
 RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840 (2001).
 CC -!- SIMILARITY: BELONGS TO THE L37E FAMILY OF RIBOSOMAL PROTEINS.
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 CC

Query Match 18.7%; Score 33.5; DB 1; Length 29;
Best Local Similarity 53.3%; Pred. No. 3e+02;

```

Matches      8;  Conservative      2;  Mismatches      2;  Indels      3;  Gaps      1;

QY 13 KHLNS---MERVEWL 24
    |||:| | | | |
Db 12 KHLDSRYAQEPVQWL 26

RESULT 13
HM09_CABEL
ID HM09_CABEL STANDARD; PRT; 60 AA.
AC PS6407;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Homeobox protein ceh-9 (Fragment).
GN CEH-9.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;

RP SEQUENCE FROM N.A.
RX MEDLINE=91045075; PubMed=1978282;
RA Hawkins N.C., McGhee J.D.;
RT "Homeobox containing genes in the nematode Caenorhabditis elegans.";
RL Nucleic Acids Res. 18:6101-6106(1990).
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; X52811; CAB57217.1; -.
DR HSSP; P14653; 1B72.
DR TRANSFAC; T02979; -.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; Hox; 1.
DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS00071; HOMEBOX 2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein.
FT NON_TER 1
FT DNA_BIND 1 60 HOMEBOX.
FT NON_TER 60
SQ SEQUENCE 60 AA; 7308 MW; 04175DFAAF5430B4 CRC64;

Query Match      18.4%; Score 33.5; DB 1; Length 60;
Best Local Similarity 37.0%; Pred. No. 6.2e+02;
Matches 10; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY 2 VSEIQLMNLGKHLNSMERVEWLKKL 28
    |||:| | | | |
Db 13 VFELEKQPEAKKYLSSDRSB-LAKRL 38

RESULT 14
PCG3_PACGO
ID PCG3_PACGO STANDARD; PRT; 30 AA.
AC B92416;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ponericin G3.
OS Pachycondyla goeldii (Ponerine ant.).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC Aculeata; Formicidae; Ponerinae; Pachycondyla.
NCBI_TaxID=118888;

[1]
SEQUENCE, AND FUNCTION.
RP TISSUE=Venom;
RX MEDLINE=21264562; PubMed=11279030;
RA Orivel J., Redeker V., Le Caer J.-P., Krier F., Revol-Junelles A.-M.,
RA Longeon A., Chafotte A., Dejean A., Rossier J.;
RT "Ponericins, new antibacterial and insecticidal peptides from the
RT venom of the ant Pachycondyla goeldii.";
RL J. Biol. Chem. 276:17823-17829(2001).
CC -1- FUNCTION: BROAD SPECTRUM OF ACTIVITY AGAINST BOTH GRAM-POSITIVE
CC AND GRAM-NEGATIVE BACTERIA AND S.CEREVISIAE. HAS INSECTICIDAL
CC AND NON-HEMOLYTIC ACTIVITIES.
CC -1- MASS SPECTROMETRY: MW=3381.36; METHOD=MALDI.
KW Antibiotic; Insect immunity; Fungicide.
SQ SEQUENCE 30 AA; 3383 MW; BC0463D0AF140B53 CRC64;

Query Match      18.4%; Score 33; DB 1; Length 30;
Best Local Similarity 44.4%; Pred. No. 3.6e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 8; Gaps 1;

QY 10 NLGKHLNSMERVEWLKKK 27
    |||:| | | | |
Db 7 NKGK-----EMLKKK 16

RESULT 15
RL7_COXBU
ID RL7_COXBU STANDARD; PRT; 36 AA.
AC OB7902;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 50S ribosomal protein L7/L12 (Fragment).
GN RPL7.
OS Coccidia burnetii.
OC Bacteria; Proteobacteria; gamma subdivision; Legionellaceae group;
OC Coccidia group; Coccidia.
NCBI_TaxID=777;

[1]
SEQUENCE FROM N.A.
RX STRAIN=Q212;
RA MEDLINE=98172740; PubMed=9511749;
RA Mollet C., Drancourt M., Raoult D.;
RT "Determination of Coccidia burnetii rpoB sequence and its use for
RT phylogenetic analysis.";
RL Gene 207:97-103(1998).

[2]
CONCEPTUAL TRANSLATION.
RA Veuthey A.-L.;
RL Unpublished observations (MAR-2000).
CC -1- FUNCTION: SEEMS TO BE THE BINDING SITE FOR SEVERAL OF THE FACTORS
CC INVOLVED IN PROTEIN SYNTHESIS AND APPEARS TO BE ESSENTIAL FOR
CC ACCURATE TRANSLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE L12P FAMILY OF RIBOSOMAL PROTEINS.
CC -1- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; A FRAMESHIFT WAS
CC INTRODUCED IN POSITION 10 TO PRODUCE THIS ORF.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U86688; AAC61665.1; ALT_FRAME.
DR InterPro; IPR000206; Ribosomal_L12.
DR Pfam; PF00542; Ribosomal_L12; 1.
KW Ribosomal protein.
FT NON_TER 1
SQ SEQUENCE 36 AA; 3930 MW; 4C1AB1ED69FB8073 CRC64;

Query Match      18.4%; Score 33; DB 1; Length 36;

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Best Local Similarity 30.8%; Pred. No. 4.3e+02;
Matches 8; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 5 IQLMHNIGKHLNSMERVEWLRKKLQD 30
Db 3 VESVPSVVKESVSKERAEKLRKSLSE 28

Search completed: April 9, 2003, 16:44:37
Job time : 18 secs

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GenCore version 5.1.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: April 9, 2003, 16:42:41 ; Search time 28 Seconds
(without alignments)

250,200 Million cell updates/sec

File: US-09-843-221A-16
Perfect score: 179
Sequence: 1 SVSEIQLMNLGKLSMERVWLKQLQDVHNF 34

Scoring table: BLOSUM62

Gap 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

1 number of hits satisfying chosen parameters: 60947

Minimum DB seq length: 0

Maximum DB seq length: 70

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SPREMBL21
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phase:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_virus:
16: sp_bacteriap:
17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	47.5	31	11 Q91Y91	Q91Y91 peromyscus
2	85	47.5	31	11 Q91Y90	Q91Y90 peromyscus
3	49.5	27.7	60	6 Q9BDL8	Q9BDL8 phocoenoid
4	47	26.3	63	10 Q9LH68	Q9LH68 arabidopsis
5	43.5	24.3	68	6 Q9BG71	Q9BG71 canis fami
6	41.5	23.2	58	5 Q94768	Q94768 strongyloce
7	41	22.9	53	7 Q30452	Q30452 equus asinu
8	40	22.3	40	5 Q27099	Q27099 trichomonas
9	40	22.3	52	8 Q35600	Q35600 paratetetic
10	40	22.3	70	4 Q9BU57	Q9BU57 homo sapien
11	39.5	22.1	54	16 Q9ZIK1	Q9ZIK1 rickettsia
12	39	21.8	40	5 Q27098	Q27098 trichomonas
13	39	21.8	52	8 Q34854	Q34854 lampronia a
14	39	21.8	70	7 Q8SNL4	Q8SNL4 rivulus mar
15	39	21.8	70	7 Q8SNL3	Q8SNL3 rivulus mar
16	39	21.8	70	7 Q8SNL0	Q8SNL0 rivulus mar

17	39	21.8	70	7 Q8SNK9	Q8SNK9 rivulus mar
18	39	21.8	70	7 Q8SNK8	Q8SNK8 rivulus mar
19	39	21.8	70	7 Q8SNK7	Q8SNK7 rivulus mar
20	39	21.8	70	7 Q8SNK6	Q8SNK6 rivulus mar
21	39	21.8	70	7 Q8SNK5	Q8SNK5 rivulus mar
22	39	21.8	70	7 Q8SNK4	Q8SNK4 rivulus mar
23	39	21.8	70	7 Q8SNK3	Q8SNK3 rivulus mar
24	39	21.8	70	7 Q8SNK2	Q8SNK2 rivulus mar
25	39	21.8	70	7 Q8SNK1	Q8SNK1 rivulus mar
26	39	21.8	70	7 Q8SNK0	Q8SNK0 rivulus mar
27	39	21.8	70	7 Q8SNJ9	Q8SNJ9 rivulus mar
28	39	21.8	70	7 Q8SNJ8	Q8SNJ8 rivulus mar
29	39	21.8	70	7 Q8SNJ7	Q8SNJ7 rivulus mar
30	39	21.8	70	7 Q8SNJ6	Q8SNJ6 rivulus mar
31	39	21.8	70	7 Q8SNJ5	Q8SNJ5 rivulus mar
32	39	21.8	70	7 Q8SNJ4	Q8SNJ4 rivulus mar
33	38.5	21.5	56	17 Q8TZD8	Q8TZD8 pyrococcus
34	38.5	21.5	61	16 Q9JUI4	Q9JUI4 neisseria m
35	38	21.2	40	5 Q27233	Q27233 trichomonas
36	38	21.2	50	2 Q8ROK9	Q8ROK9 bacillus ce
37	38	21.2	52	8 Q34628	Q34628 greya powel
38	38	21.2	52	8 Q34680	Q34680 greya varia
39	38	21.2	56	16 Q8RAP7	Q8RAP7 thermoanaer
40	38	21.2	61	2 Q9X9G5	Q9X9G5 yersinia ps
41	38	21.2	68	16 Q8X414	Q8X414 escherichia
42	37.5	20.9	45	5 Q94693	Q94693 polycelis n
43	37.5	20.9	58	16 Q8XLW5	Q8XLW5 clostridium
44	37.5	20.9	69	17 Q26627	Q26627 methanobact
45	37	20.7	48	7 Q98171	Q98171 melopsittac

ALIGNMENTS

RESULT 1

Q91Y91 ID Q91Y91 PRELIMINARY; PRT; 31 AA.

AC Q91Y91;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Parathyroid hormone (Fragment).
GN PTH.

OS Peromyscus polionotus (Oldfield mouse).
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Peromyscus.

OX NCBI_TaxID=42413;

RN [1] SEQUENCE FROM N.A.

RP PRINCE K.L., Dewey M.J.;

RA Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.

RL EMBL; AF382952; AAK63071.1;

DR InterPro; IPR001415; Parathyrd.hrm.

DR InterPro; IPR003625; Pthyrdorm_sub.

DR Pfam; PF01279; Parathyroid; 1.

DR ProDom; PD010687; Pthyrdorm sub; 1.

DR PROSITE; PS00335; PARATHYROID; UNKNOWN_1.

FT NON_TER 1 1

FT NON_TER 31 31

SQ SEQUENCE 31 AA; 3461 MW; A208B0E772B9B55B CRC64;

Query Match 47.5%; Score 85; DB 11; Length 31;

Best Local Similarity 89.5%; Pred. No. 0.00027;

Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQLMNLGKLSMERVWLKQLQDVHNF 19

Db 13 AVSEIQLMNLGKLSMERVWLKQLQDVHNF 31

RESULT 2

Q91Y90

```

ID Q91Y90 PRELIMINARY; PRT; 31 AA.
AC Q91Y90;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Parathyroid hormone (Fragment).
GN PTH.
OS Peromyscus maniculatus (Deer mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Peromyscus.
OX NCBI_TaxID=10042;
RN [1]
RP SEQUENCE FROM N.A.
RA Prince K.L., Dewey M.J.; to the EMBL/GenBank/DBJ databases.
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF382953; AAK63072.1; -.
DR InterPro; IPR001415; Parathyroid_hrm.
DR InterPro; IPR003625; Pthyrohm_sub.
DR Pfam; PF01279; Parathyroid; 1.
DR ProDom; PD010687; Pthyrohm_sub; 1.
FT PROSITE; PS00335; PARATHYROID; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 31
SQ SEQUENCE 31 AA; 3461 MW; A208B0E772B9B55B CRC64;

Query Match 47.5%; Score 85; DB 11; Length 31;
Best Local Similarity 89.5%; Pred. No. 0.00027;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSME 19
Db :|||||
13 AVSEIQLMHNLGKHLASME 31

RESULT 3
Q9BDL8 PRELIMINARY; PRT; 60 AA.
ID Q9BDL8;
AC Q9BDL8;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Interleukin-10 (Fragment).
OS Phocoenoides phocoena (Harbor porpoise).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Phocoenidae;
OC Phocoena.
OX NCBI_TaxID=9742;
RN [1]
RP SEQUENCE FROM N.A.
RA Beineke A., Groene A., Baumgaertner W.;
RT "Detection of interleukin-10 mRNA in concanavalin A-stimulated
peripheral blood lymphocytes of the harbor porpoise."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF346234; AAK19739.1; -.
DR HSSP; P22301; 1INR.
DR InterPro; IPR000098; Interleukin_10.
DR Pfam; PF00726; IL10; 1.
DR ProDom; PD003687; Interleukin_10; 1.
DR SMART; SM00188; IL10; 1.
FT NON_TER 1
FT NON_TER 60
SQ SEQUENCE 60 AA; 7063 MW; 90EFD2DA955D8BF4 CRC64;

Query Match 27.7%; Score 49.5; DB 6; Length 60;
Best Local Similarity 38.5%; Pred. No. 26;
Matches 10; Conservative 9; Mismatches 6; Indels 1; Gaps 1;

QY 10 NLGKHLNSM-ERVEWLKRLQDVHNF 34
Db :|||||
19 NIKHVNLSGKLTURLRLRCHRF 44

us-09-843-221a-16.rspt
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RESULT 4
Q9LH68 PRELIMINARY; PRT; 63 AA.
ID Q9LH68;
AC Q9LH68;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE Gb|AAD27902.1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=COLUMBIA;
RA Nakamura Y.;
RT "Structural Analysis of Arabidopsis thaliana Chromosome 3. III.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP002062; BAB02653.1; -.
DR PROSITE; PS00335; PARATHYROID; UNKNOWN_1.
SQ SEQUENCE 63 AA; 7025 MW; 2C8966DDEB4673DD CRC64;

Query Match 26.3%; Score 47; DB 10; Length 63;
Best Local Similarity 47.1%; Pred. No. 57;
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 7 LMHNLGKHLNSMERVEW 23
Db :|||||
38 LLNLLGKHPNKVIQTVW 54

RESULT 5
Q9BG71 PRELIMINARY; PRT; 68 AA.
ID Q9BG71;
AC Q9BG71;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Interleukin 10 (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Markus S., Groene A., Baumgaertner W.;
RT "Expression of canine interleukin-10 mRNA in concanavalin A-stimulated
canine lymphocytes."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF333120; AAK01440.1; -.
DR HSSP; P22301; 1INR.
DR InterPro; IPR000098; Interleukin_10.
DR Pfam; PF00726; IL10; 1.
DR ProDom; PD003687; Interleukin_10; 1.
DR SMART; SM00188; IL10; 1.
DR PROSITE; PS00520; INTERLEUKIN_10; 1.
FT NON_TER 1
FT NON_TER 68
SQ SEQUENCE 68 AA; 7920 MW; AF916BEB1EAA438C CRC64;

Query Match 24.3%; Score 43.5; DB 6; Length 68;
Best Local Similarity 34.6%; Pred. No. 1.8e+02;
Matches 9; Conservative 9; Mismatches 7; Indels 1; Gaps 1;

QY 10 NLGKHLNSM-ERVEWLKRLQDVHNF 34
Db :|||||
27 DIKNHVNLSGKLTURLRLRCHRF 52

RESULT 6
Q94768 PRELIMINARY; PRT; 58 AA.
ID Q94768
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Q94768;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Rabl1 GTPase homolog SURABIP (Fragment).
 OS Strongylocentrotus purpuratus (Purple sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Euechinozoa; Echinacea; Echinoida; Strongylocentrotidae;
 OC Strongylocentrotus.
 OX NCBI_TaxID=7668;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Leaf D.S.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U88769; BAB09700.1; --
 DR HSSP; P17080; IAKZ.
 DR InterPro; IPR001806; Ras trnsfrmg.
 DR InterPro; IPR003575; Small_GTPase.
 DR Pfam; PF00071; ras; 1.
 DR SMART; SM00010; small_GTPase; 1.
 FT NON_TER 1 58
 FT NON_TER 58 58
 SQ SEQUENCE 58 AA; 6770 MW; 09086186050D76E3 CRC64;
 Query Match 23.2%; Score 41.5; DB 5; Length 58;
 Best Local Similarity 48.0%; Pred. No. 2.8e+02;
 Matches 12; Conservative 7; Mismatches 3; Indels 3; Gaps 3;
 QY 7 LMENLGNLNSMERVE-WLRKKLQD 30
 DB 20 LVYDIAGHL-TYENVERWL-KELRD 42
 RESULT 7
 Q30452
 ID Q30452 PRELIMINARY; PRT; 53 AA.
 AC Q30452;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MHC class II HLA-DOB1 antigen (Fragment).
 OS Equus asinus (Donkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9793;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nasir L., Stear M.J., Reid S.W.J.;
 "Nucleotide sequence of the Donkey MHC DOB first domain exon."
 Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U31774; AAA86414.1; --
 DR InterPro; IPR000353; MHC_II_beta.
 DR Pfam; PF00969; MHC_II_beta; 1.
 DR ProDom; PD000328; MHC_II_beta; 1.
 KW Glycoprotein; MHC II; Transmembrane.
 FT NON_TER 1 53
 FT NON_TER 53 53
 SQ SEQUENCE 53 AA; 6406 MW; 9DA1C857BC30DDA1 CRC64;
 Query Match 22.9%; Score 41; DB 7; Length 53;
 Best Local Similarity 34.6%; Pred. No. 3e+02;
 Matches 9; Conservative 5; Mismatches 8; Indels 4; Gaps 1;
 QY 2 VSEIQLMHNGLKHLNSMERVEWLRKK 27
 DB 24 VGEFQAVTELGRHIAE----DWNQK 45
 RESULT 8
 Q27099
 ID Q27099 PRELIMINARY; PRT; 40 AA.
 AC Q27099;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Ubiquitin (Fragment).
 GN UBI.
 OS Trichomonas vaginalis.
 OC Eukaryota; Parabasalidea; Trichomonadida; Trichomonadidae;
 OC Trichomonas.
 OX NCBI_TaxID=5722;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NIH-C1;
 RA Keeling P.J., Doolittle W.F.;
 RL "Concerted evolution in protists: recent homogenization of a polyubiquitin gene in Trichomonas vaginalis."
 J. Mol. Evol. 41:556-562(1995).
 DR EMBL; U28011; AAC46939.1; --
 DR HSSP; P02248; UBI.
 DR InterPro; IPR000626; Ubiquitin.
 DR Pfam; PF00240; ubiquitin; 1.
 DR PROSITE; PS50053; UBIQUITIN_2; 1.
 FT NON_TER 1 40
 FT NON_TER 40 40
 SQ SEQUENCE 40 AA; 4530 MW; 5ADDA65EEEC2DALA CRC64;
 Query Match 22.3%; Score 40; DB 5; Length 40;
 Best Local Similarity 34.8%; Pred. No. 3e+02;
 Matches 8; Conservative 7; Mismatches 4; Indels 4; Gaps 1;
 QY 12 GKHL-----NSMERVEWLRKKLQD 30
 DB 4 GKHLTVESADKIEDVKAKIQD 26
 RESULT 9
 Q35600
 ID Q35600 PRELIMINARY; PRT; 52 AA.
 AC Q35600;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Cytochrome oxidase subunit I (Fragment).
 OS Parategetica pollenifera.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
 OC Incurvarioidea; Prodoxidae; Parategetica.
 OX NCBI_TaxID=30238;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SANTA CRUZ CO;
 RA Brown J.M., Pellmyr O., Thompson J.N., Harrison R.G.;
 RT "Mitochondrial DNA phylogeny of the Prodoxidae (Lepidoptera: Incurvarioidea) indicates rapid ecological diversification of yucca moths."
 Ann. Entomol. Soc. Amer. 87:795-802(1994).
 DR EMBL; U04884; AAA16151.1; --
 KW Mitochondrion.
 FT NON_TER 1 52
 FT NON_TER 52 52
 SQ SEQUENCE 52 AA; 6105 MW; C4E2ED2351EC5ED1 CRC64;
 Query Match 22.3%; Score 40; DB 8; Length 52;
 Best Local Similarity 35.0%; Pred. No. 3.9e+02;
 Matches 7; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
 QY 15 LNSMERVEWLRKKLQDVNF 34
 DB 24 LNTSSIEWLQKFPPTHEYS 43
 RESULT 10
 Q9BU57
 ID Q9BU57 PRELIMINARY; PRT; 70 AA.

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AC Q9BU57;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Similar to cofactor required for Spl transcriptional activation,
DE subunit 8 (34kd).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Srausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002878; AA02878.1; -.
SQ SEQUENCE 70 AA; 8019 MW; 83AC87EA4760E384 CRC64;

Query Match 22.3%; Score 40; DB 4; Length 70;
Best Local Similarity 32.0%; Pred. No. 5.3e+02;
Matches 8; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Qy 8 MHNLGKHLNSMERVWLKKLQDVH 32
   : : : : : : : : : : : : : :
Db 22 LHSVNRDLNELRLSLNVLGKPSNH 46

RESULT 11
ID Q92IK1 PRELIMINARY; PRT; 54 AA.
AC Q92IK1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical protein RC0419.
GN RC0419.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsieae; Rickettsia.
OX NCBI_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MALISH 7;
RX MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA Sanson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RA Raoult D.;
RA "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
Science 293:2093-2098(2001).
DR EMBL; AB008606; AA02957.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 54 AA; 6120 MW; 063655E7022C28C0 CRC64;

Query Match 22.1%; Score 39.5; DB 16; Length 54;
Best Local Similarity 37.0%; Pred. No. 4.8e+02;
Matches 10; Conservative 7; Mismatches 9; Indels 1; Gaps 1;

Qy 5 IQLMNLGKHLNSMERVWLKKLQDV 31
   : : : : : : : : : : : : : :
Db 15 IEVVMYIFGHLNS-EKSTVSCKKVTET 40

RESULT 12
Q27098
ID Q27098 PRELIMINARY; PRT; 40 AA.
AC Q27098;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Ubiquitin (Fragment).
GN UBI1.
OS Trichomonas vaginalis.
OC Eukaryota; Parabasalidae; Trichomonadida; Trichomonadidae;

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OC Trichomonas.
OX NCBI_TaxID=5722;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NIH-C1;
RX MEDLINE=96081479; PubMed=7490769;
RA Keeling P.J., Doolittle W.F.;
RA "Concerted evolution in protists: recent homogenization of a
RA polyubiquitin gene in Trichomonas vaginalis.";
RL J. Mol. Evol. 41:556-562(1995).
DR EMBL; U28008; AAC46936.1; -.
DR HSSP; P02248; 1UBI.
DR InterPro; IPR00626; Ubiquitin.
DR Pfam; PF00240; ubiquitin; 1.
DR PROSITE; PS50053; UBIQUITIN_2; 1.
FT NON_TER 1
FT NON_TER 40
SQ SEQUENCE 40 AA; 4528 MW; 46843B0C9BF0E7EA CRC64;

Query Match 21.8%; Score 39; DB 5; Length 40;
Best Local Similarity 34.8%; Pred. No. 4.1e+02;
Matches 8; Conservative 6; Mismatches 5; Indels 4; Gaps 1;

Qy 12 GKHL----NSMERVWLKKLQD 30
   : : : : : : : : : : : : : :
Db 4 GKHTLEVEPTDRIEVVKAKIQD 26

RESULT 13
Q34854
ID Q34854 PRELIMINARY; PRT; 52 AA.
AC Q34854;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cytochrome oxidase subunit I (Fragment).
OS Lampronia aenesens.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
OC Incurvarioidea; Prodoxidae; Lampronia.
OX NCBI_TaxID=30234;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GARFIELD CO;
RA Brown J.M., Fellmyr O., Thompson J.N., Harrison R.G.;
RA "Mitochondrial DNA phylogeny of the Prodoxidae (Lepidoptera:
RA Incurvarioidea) indicates rapid ecological diversification of yucca
RA moths.";
RL Ann. Entomol. Soc. Amer. 87:795-802(1994).
DR EMBL; U04889; AAA16085.1; -.
KW Mitochondrion.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 52 AA; 6043 MW; 45BA2FC4FE22B094 CRC64;

Query Match 21.8%; Score 39; DB 8; Length 52;
Best Local Similarity 30.0%; Pred. No. 5.3e+02;
Matches 6; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 15 LNSMERVWLKKLQDVHNF 34
   : : : : : : : : : : : : : :
Db 24 LNTISIEWLQNSPPAEHSY 43

RESULT 14
Q8SNL4
ID Q8SNL4 PRELIMINARY; PRT; 70 AA.
AC Q8SNL4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE MHC class I antigen (Fragment).
OS Rivulus marmoratus (mangrove rivulus).

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Result No.	Score	Query Match	Length	DB	ID	Description
1	179	100.0	34	9	US-09-928-0478-6	Sequence 6, Appl
2	179	100.0	34	9	US-09-843-221A-16	Sequence 16, Appl
3	179	100.0	34	9	US-09-843-221A-16	Sequence 16, Appl
4	179	100.0	34	10	US-09-169-786-3	Sequence 3, Appl
5	179	100.0	34	12	US-10-016-403-5	Sequence 5, Appl
6	179	100.0	34	12	US-10-037-079-1	Sequence 1, Appl
7	179	100.0	38	9	US-09-843-221A-14	Sequence 14, Appl
8	179	100.0	38	10	US-09-169-786-4	Sequence 4, Appl
9	179	100.0	42	9	US-10-024-918-28	Sequence 28, Appl
10	179	100.0	44	9	US-09-843-221A-13	Sequence 13, Appl
11	175	97.8	34	9	US-09-843-221A-10	Sequence 20, Appl
12	175	97.8	37	9	US-09-843-221A-10	Sequence 15, Appl
13	174	97.2	34	9	US-09-843-221A-19	Sequence 19, Appl
14	174	97.2	34	9	US-09-843-221A-164	Sequence 164, Appl
15	174	97.2	34	12	US-10-016-403-5	Sequence 6, Appl
16	174	97.2	34	12	US-10-036-403-7	Sequence 7, Appl
17	173	96.6	34	9	US-09-843-221A-17	Sequence 17, Appl
18	173	96.6	34	9	US-09-843-221A-18	Sequence 18, Appl
19	173	96.6	34	9	US-09-843-221A-162	Sequence 162, Appl

RESULT 2
US-09-843-221A-16
; Sequence 16, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-PA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RE
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/84

; CURRENT FILING DATE: 2001-04-26
 ; PRIOR APPLICATION NUMBER: 60/266,673
 ; PRIOR FILING DATE: 2001-02-06
 ; PRIOR APPLICATION NUMBER: 60/214,860
 ; PRIOR FILING DATE: 2000-06-28
 ; PRIOR APPLICATION NUMBER: 60/200,053
 ; PRIOR FILING DATE: 2000-04-27
 ; NUMBER OF SEQ ID NOS: 170
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 16
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-843-221A-16

Query Match 100.0%; Score 179; DB 9; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.9e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 SVSEIQLMHNLGKHLNSMERVWLRKKLQDVHNF 34
 1 SVSEIQLMHNLGKHLNSMERVWLRKKLQDVHNF 34

RESULT 3
 US-09-843-221A-161
 ; Sequence 161, Application US/09843221A
 ; Publication No. US20030039654A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KOSTENIUK, PAUL
 ; APPLICANT: LIU, CHUAN-PA
 ; APPLICANT: LACEY, DAVID LEE
 ; TITLE OF INVENTION: MODULATORS OF RECEPTORS
 ; TITLE OF INVENTION: RELATED PROTEIN
 ; FILE REFERENCE: A-665B
 ; CURRENT APPLICATION NUMBER: US/09/843,221A
 ; CURRENT FILING DATE: 2001-04-26
 ; PRIOR APPLICATION NUMBER: 60/266,673
 ; PRIOR FILING DATE: 2001-02-06
 ; PRIOR APPLICATION NUMBER: 60/214,860
 ; PRIOR FILING DATE: 2000-06-28
 ; PRIOR APPLICATION NUMBER: 60/200,053
 ; PRIOR FILING DATE: 2000-04-27
 ; NUMBER OF SEQ ID NOS: 170
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 161
 ; LENGTH: 34
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence

; FEATURE:
 ; OTHER INFORMATION: Preferred embodiments - PTH
 ; NAME/KEY: misc feature
 ; LOCATION: (34)-(34)
 ; OTHER INFORMATION: Optional linker and PC domain attached at the C-terminus
 US-09-843-221A-161

Query Match 100.0%; Score 179; DB 9; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.9e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SVSEIQLMHNLGKHLNSMERVWLRKKLQDVHNF 34
 Db 1 SVSEIQLMHNLGKHLNSMERVWLRKKLQDVHNF 34

RESULT 4
 US-09-169-786-3
 ; Sequence 3, Application US/09169786B
 ; Patent No. US20020025929A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sato, Masahiko
 ; TITLE OF INVENTION: METHOD OF BUILDING AND MAINTAINING BONE
 ; FILE REFERENCE: X-11480

; CURRENT APPLICATION NUMBER: US/09/169,786B
 ; CURRENT FILING DATE: 1998-10-09
 ; EARLIER APPLICATION NUMBER: US 60/061,800
 ; EARLIER FILING DATE: 1997-10-14
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: Patent in Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 34
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-169-786-3

Query Match 100.0%; Score 179; DB 10; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.9e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SVSEIQLMHNLGKHLNSMERVWLRKKLQDVHNF 34
 Db 1 SVSEIQLMHNLGKHLNSMERVWLRKKLQDVHNF 34

RESULT 5
 US-10-016-403-5
 ; Sequence 5, Application US/10016403
 ; Patent No. US20020107505A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Holladay, Leslie A.
 ; TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE DRUGS TO
 ; INCREASE ELECTROTRANSPORT FLUX
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Stroud, Stroud, Willink, Thompson & Howard
 ; STREET: 25 West Main Street
 ; CITY: Madison
 ; STATE: WI
 ; COUNTRY: USA
 ; ZIP: 53701-2236

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/016,403
 ; FILING DATE: 10-Dec-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/466,610
 ; FILING DATE: 1995-JUN-06
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Frenchick, Grady J.
 ; REGISTRATION NUMBER: 29,018
 ; REFERENCE/DOCKET NUMBER: 8734.28
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 608-257-2281
 ; TELEFAX: 608-257-7643

; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 34 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; FEATURE:
 ; NAME/KEY: Peptide
 ; LOCATION: 1..34
 ; OTHER INFORMATION: /note= "parathyroid hormone"
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 US-10-016-403-5

Query Match 100.0%; Score 179; DB 12; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.9e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SVSEIQLMHNLGKHLNSMERVWLRKKLQDVHNF 34

Db 1 SVSEIQLMHNGLGKHLNSMERVEWLKQLQDVHNF 34
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RESULT 6
US-10-097-079-1
; Sequence 1, Application US/10097079
; Patent No. US20020132973A1
; GENERAL INFORMATION:
; APPLICANT: Condon, Stephen M.
; ; Morize, Isabelle
; TITLE OF INVENTION: PEPTIDE PARATHYROID HORMONE ANALOGS
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, Mailstop 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/097,079
; FILING DATE: 13-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/228,990
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 60/046,472
; FILING DATE: 14-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Martin Esq., Michael B.
; REGISTRATION NUMBER: 37,521
; REFERENCE/DOCKET NUMBER: A2678B-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-2793
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: NO. US20020132973A1 Relevant
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
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US-10-097-079-1
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Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SVSEIQLMHNGLGKHLNSMERVEWLKQLQDVHNF 34
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Db 1 SVSEIQLMHNGLGKHLNSMERVEWLKQLQDVHNF 34
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RESULT 7
US-09-843-221a-14
; Sequence 14, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENIUK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A

; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 14
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221a-14
Query Match 100.0%; Score 179; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.1e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SVSEIQLMHNGLGKHLNSMERVEWLKQLQDVHNF 34
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Db 1 SVSEIQLMHNGLGKHLNSMERVEWLKQLQDVHNF 34
|||
RESULT 8
US-09-169-786-4
; Sequence 4, Application US/09169786B
; Patent No. US2002025929A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Masahiko
; TITLE OF INVENTION: METHOD OF BUILDING AND MAINTAINING BONE
; FILE REFERENCE: X-11480
; CURRENT APPLICATION NUMBER: US/09/169,786B
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,800
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 4
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-169-786-4
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Best Local Similarity 100.0%; Pred. No. 2.1e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 SVSEIQLMHNGLGKHLNSMERVEWLKQLQDVHNF 34
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RESULT 9
US-10-024-918-28
; Sequence 28, Application US/10024918
; Patent No. US20020168718A1
; GENERAL INFORMATION:
; APPLICANT: Hubbell, Jeffrey
; APPLICANT: Schense, Jason
; APPLICANT: Zisch, Andreas
; APPLICANT: Hall, Heike
; TITLE OF INVENTION: ENZYME-MEDIATED MODIFICATION OF FIBRIN FOR TISSUE ENGINEERING
; FILE REFERENCE: CIT 2606 CIP
; CURRENT APPLICATION NUMBER: US/10/024,918
; CURRENT FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 28
; LENGTH: 42
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:


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; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-19

Query Match          97.2%; Score 174; DB 9; Length 34;
Best Local Similarity 97.1%; Pred. No. 8.7e-17;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNIGKHLNSMERVWLRKKLQDVHNF 34
Db 1 SVSEIQLMHNIGKHLNSMERVWLRKKLQDVHNF 34

RESULT 14
US-09-843-221A-164
; Sequence 164, Application US/09843221A
; Publication No. US20030039654A1
; SERIAL INFORMATION:
; APPLICANT: KOSTENIUK, PAUL
; APPLICANT: LIU, CHUAN-PA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 164
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc feature
; LOCATION: (34)..(34)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-164

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Best Local Similarity 97.1%; Pred. No. 8.7e-17;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNIGKHLNSMERVWLRKKLQDVHNF 34
Db 1 SVSEIQLMHNIGKHLNSMERVWLRKKLQDVHNF 34

RESULT 15
US-10-016-403-6
; Sequence 6, Application US/10016403
; Patent No. US20020107505A1
; GENERAL INFORMATION:
; APPLICANT: Holladay, Leslie A.
; TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE DRUGS TO
; INCREASE ELECTROTRANSPORT FLUX
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stroud, Stroud, Willink, Thompson & Howard
; STREET: 25 West Main Street
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53701-2236

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/016,403
; FILING DATE: 10-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466,610
; FILING DATE: 1995-JUN-06
; ATTORNEY/AGENT INFORMATION:
; NAME: Frenchick, Grady J.
; REGISTRATION NUMBER: 29,018
; REFERENCE/DOCKET NUMBER: 8734.28
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-257-2281
; TELEFAX: 608-257-7643
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..34
; OTHER INFORMATION: /note= "modified parathyroid
; hormone"
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-016-403-6

Query Match          97.2%; Score 174; DB 12; Length 34;
Best Local Similarity 97.1%; Pred. No. 8.7e-17;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNIGKHLNSMERVWLRKKLQDVHNF 34
Db 1 SVSEIQLMHNIGKHLNSMERVWLRKKLQDVHNF 34

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Job time : 15 secs

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GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: April 9, 2003, 16:43:07 ; Search time 17 Seconds
(without alignments)
192.269 Million cell updates/sec

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Searched: 283224 seqs, 96134422 residues

Number of hits satisfying chosen parameters: 20812

Minimum DB seq length: 0
Maximum DB seq length: 70

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: us-09-843-221a-16
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3: Pir3: *
4: Pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	22.3	57	C53260	hypothetical prote
2	39.5	22.1	54	C97752	hypothetical prote
3	39	21.8	70	A23809	160K antigen - mal
4	38.5	21.5	61	A81898	hypothetical prote
5	38	21.2	55	S43483	hypothetical prote
6	38	21.2	60	D44088	homeotic protein H
7	38	21.2	61	T47055	hypothetical prote
8	38	21.2	68	F85909	hypothetical prote
9	37.5	20.9	69	E69169	hypothetical prote
10	37	20.7	61	C69260	hypothetical prote
11	37	20.7	62	A12130	hypothetical prote
12	37	20.7	64	B69175	hypothetical prote
13	36	20.1	55	A84180	hypothetical prote
14	36	20.1	68	G82027	hypothetical prote
15	36	20.1	70	E90872	hypothetical prote
16	36	20.1	70	F85746	unknown protein en
17	35.5	19.8	34	G84147	hypothetical prote
18	35.5	19.8	40	S71295	deoxyguanosine kin
19	35.5	19.8	52	T00141	hypothetical prote
20	35.5	19.8	54	S22948	SOX-13 protein - A
21	35	19.6	51	C69153	hypothetical prote
22	35	19.6	52	S52069	hypothetical prote
23	35	19.6	58	AH1092	hypothetical prote
24	35	19.6	60	A34945	transcription regu
25	35	19.6	61	AH3198	hypothetical prote
26	34.5	19.3	51	A56785	calmodulin - pig
27	34.5	19.3	59	H82107	hypothetical prote
28	34.5	19.3	61	E90224	150 ribosomal prote
29	34.5	19.3	65	S35024	hypothetical prote

30 34.5 19.3 69 2 S14074
31 34 19.0 34 2 T46886
32 34 19.0 44 2 B43714
33 34 19.0 44 2 T26815
34 34 19.0 49 2 S70651
35 34 19.0 57 2 C35058
36 34 19.0 60 2 T03132
37 34 19.0 60 2 AF2104
38 34 19.0 63 2 T12637
39 34 19.0 65 2 AE2554
40 34 19.0 68 2 A32425
41 33.5 18.7 29 1 GCCB
42 33.5 18.7 50 2 C72806
43 33.5 18.7 54 2 AE2925
44 33.5 18.7 60 2 S13129
45 33.5 18.7 63 2 A10730

ALIGNMENTS

RESULT 1

C53260
hypothetical protein (clone N40) - Norwalk virus (fragment)
C;Species: Norwalk virus

C;Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 26-May-2000
C;Accession: C53260

R;Matsui, S.M.; Kim, J.P.; Greenberg, H.B.; Su, W.; Sun, Q.; Johnson, P.C.; DuPont, H.L
J. Clin. Invest. 87, 1456-1461, 1991

A;Title: The isolation and characterization of a norwalk virus-specific cDNA.

A;Reference number: A53260; MUID:91185631; PMID:2010555

A;Accession: C53260

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-57 <MAT>

C;Superfamily: rabbit calicivirus RNA-directed RNA polymerase

Query Match 22.3%; Score 40; DB 2; Length 57;
Best Local Similarity 42.9%; Pred. No. 2.4e+02;

Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 8 MHNGLGHLNSMERVWLKQL 28
DB 30 MASLGKLRSVTTIEGLKNAL 50

RESULT 2

C97752

hypothetical protein RC0419 [imported] - Rickettsia conorii (strain Malish 7)

C;Species: Rickettsia conorii

C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001

C;Accession: C97752

R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; R

Science 293, 2093-2098, 2001

A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.

A;Reference number: A97700; MUID:21442074; PMID:11557893

A;Accession: C97752

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-54 <KUR>

A;Cross-references: GB:AE006914; PIDN:AL02957.1; PID:gl5619488; GSPDB:GN00173

C;Genetics:

A;Gene: RC0419

Query Match 22.1%; Score 39.5; DB 2; Length 54;

Best Local Similarity 37.0%; Pred. No. 2.4e+02;

Matches 10; Conservative 7; Mismatches 9; Indels 1; Gaps 1;

QY 5 IQLMNLGHLNSMERVWLKQLQDV 31
DB 15 IEVWHYIFGHLNS-EKSTVSSKKVTEI 40

RESULT 3

A23809
160K antigen - malaria parasite (Plasmodium falciparum) (fragments)
C;Species: Plasmodium falciparum
C;Date: 20-Aug-1987 #sequence_revision 20-Aug-1987 #text_change 09-Jun-2000
C;Accession: A23809; A05268
R;Langley, G.; Scherf, A.; Mercereau-Puijalon, O.; Koenen, M.; Kahane, B.; Mattei, D.; Nucleic Acids Res. 13, 4191-4202, 1985
A;Title: Characterization of Plasmodium falciparum antigenic determinants isolated from A;Reference number: A93570; MUID:85242097; PMID:2409532
A;Accession: A23809
A;Molecule type: DNA
A;Residues: 1-70 <LAN>
A;Experimental source: clone ppp2L
C;Comment: This antigen is expressed in all blood stages.
C;Keywords: surface antigen

Query Match 21.8%; Score 39; DB 2; Length 70;
Best Local Similarity 39.1%; Pred. No. 3.6e+02;
Matches 9; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 5 IQLMHNIGKHLNSMERVEWLKQDVHNF 27

Db 10 IYILNNIKNLKENVDLNKR 32

RESULT 4

A81898
hypothetical protein NMA1295 [imported] - Neisseria meningitidis (strain 22491 serogroup C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: A81898
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel; Holroyd, S.; Jägle, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491.
A;Reference number: A81775; MUID:2022556; PMID:10761919
A;Accession: A81898
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-61 <PAR>
A;Cross-references: GB:AL162755; GB:AL157959; NID:G7379742; PIDN:CAB84547.1; PID:G737997
A;Experimental source: serogroup A, strain 22491
C;Genetics:
A;Gene: NMA1295

Query Match 21.5%; Score 38.5; DB 2; Length 61;
Best Local Similarity 30.0%; Pred. No. 3.6e+02;
Matches 9; Conservative 9; Mismatches 11; Indels 1; Gaps 1;

QY 6 QLMNIGKHLNSMERVEWLKQDVHNF 34

Db 22 RLKTVSPHLERKELVDFMQKEIPDFSNW 51

RESULT 5

S43483
hypothetical protein - Escherichia coli (fragment)
C;Species: Escherichia coli
C;Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 01-Feb-1999
C;Accession: S43483
R;Knopp, V.; Brennick, A.
Nucleic Acids Res. 22, 1167-1171, 1994
A;Title: Evidence for a group II intron in Escherichia coli inserted into a highly conserved A;Reference number: S43481; MUID:94218238; PMID:8165129
A;Accession: S43483
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-55 <KNO>

Query Match 21.2%; Score 38; DB 2; Length 55;
Best Local Similarity 30.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 15 LNSMERVEWLKQDVHNF 34

Db 22 LNNVEPKWLRVYVIEHQDW 41

RESULT 6

D44088
homeotic protein HAT24 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 27-Jun-1994
C;Accession: D44088
R;Schna, M.; Davis, R.W.
Proc. Natl. Acad. Sci. U.S.A. 89, 3894-3898, 1992
A;Title: HD-Zip proteins: members of an Arabidopsis homeodomain protein superfamily.
A;Reference number: A44088; MUID:92237275; PMID:1349174
A;Accession: D44088
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-60 <SCH>
A;Cross-references: GB:M90418

Query Match 21.2%; Score 38; DB 2; Length 60;
Best Local Similarity 29.6%; Pred. No. 4.1e+02;
Matches 8; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 7 LMHNIGKHLNSMERVEWLKQDVHNF 33

Db 5 MNENIEKVLDRGEKIELLVDTENLRS 31

RESULT 7

T47055
hypothetical protein [imported] - Yersinia pestis
C;Species: Yersinia pestis
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C;Accession: T47055
R;Buchrieser, C.; Rusniok, C.; Couve, E.; Frangeul, L.; Billault, A.; Kunst, F.; Carnie submitted to the EMBL Data Library, October 1998
A;Description: DNA sequence of the 102 kbases unstable region of Yersinia pestis.
A;Reference number: Z24348
A;Accession: T47055
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-61 <BUC>
A;Cross-references: EMBL:AL031866; PIDN:CAA21398.1
A;Experimental source: strain 6/69

Query Match 21.2%; Score 38; DB 2; Length 61;
Best Local Similarity 66.7%; Pred. No. 4.2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 22 EWLKQDVHNF 30

Db 52 EWINKLSD 60

RESULT 8

F85909
hypothetical protein Z3923 [imported] - Escherichia coli (strain O157:H7, substrain ED1 C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: F85909
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: F85909
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-68 <STO>
A;Cross-references: GB:AE005174; NID:gl2517055; PIDN:AAG57738.1; GSPDB:GN00145; UWGP:Z3

A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z3923

Query Match 21.2%; Score 38; DB 2; Length 68;
Best Local Similarity 25.0%; Pred. No. 4.7e+02;
Matches 7; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 6 QLMHNLGKHLNSMERVWLKRLQDVHN 33
DB 32 QQRHPDKRSARQHDWLRKREIQRYVD 59

RESULT 9
E69169
hypothetical protein MTH527 - Methanobacterium thermoautotrophicum (strain Delta H)
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C;Accession: E69169
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiواني, N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: E69169
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-69 <MTH>
A;Cross-references: GB:AE000835; GB:AE000666; NID:g2621586; PIDN:AAB85033.1; PID:g262160
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH527
A;Start codon: GTG

Query Match 20.9%; Score 37.5; DB 2; Length 69;
Best Local Similarity 25.9%; Pred. No. 5.6e+02;
Matches 7; Conservative 12; Mismatches 7; Indels 1; Gaps 1;

QY 5 IQLMHNLGKHLNSMERVWLKRLQDVHN 30
DB 40 LEILNVGKLEEDVLDLLEETEE 66

RESULT 10
C69260
hypothetical protein AF0083 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C;Accession: C69260
R;Fleischmann, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
J. Bacteriol. 179, 7135-7155, 1997
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: C69260
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-61 <KLE>
A;Cross-references: GB:AE001100; GB:AE000782; NID:g2689423; PIDN:AAB91149.1; PID:g2625056

Query Match 20.7%; Score 37; DB 2; Length 61;
Best Local Similarity 46.2%; Pred. No. 5.7e+02;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 VSEIQLMNLGKHL 14
DB 21 ISKPRLIHQTKH 33

RESULT 11
AI2130
hypothetical protein asr2600 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp.
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C;Accession: AI2130
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Itiguch
Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AI2130
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-62 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAW74299.1; PID:gl7131693; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: asr2600

Query Match 20.7%; Score 37; DB 2; Length 62;
Best Local Similarity 36.4%; Pred. No. 5.8e+02;
Matches 8; Conservative 7; Mismatches 5; Indels 2; Gaps 1;

QY 12 GKHLNSMERVWLKRLQDVHN 33
DB 27 GLHLSYEQLRLVREQIQ--HN 46

RESULT 12
B69175
hypothetical protein MTH568 - Methanobacterium thermoautotrophicum (strain Delta H)
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C;Accession: B69175
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiواني, N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: B69175
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-64 <MTH>
A;Cross-references: GB:AE000839; GB:AE000666; NID:g2621637; PIDN:AAB85074.1; PID:g26216
A;Experimental source: strain Delta H
C;Genetics:
A;Start codon: GTG

Query Match 20.7%; Score 37; DB 2; Length 64;
Best Local Similarity 38.1%; Pred. No. 5.9e+02;
Matches 8; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 6 QLMHNLGKHLNSMERVWLKRL 26
DB 42 RLELLSTHPNMLKRVRLSK 62

RESULT 13
B84180
hypothetical protein Vng0194h [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: B84180
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Title: Genome sequence of Halobacterium species NRC-1.

[illegible]

Key	Location/Qualifiers
34	
Modified-site	/note= "amidated"
XX	
XX	
PN	JP58096052-A.
XX	
PD	07-JUN-1983.
XX	
XX	30-NOV-1983; 83JP-01933212.
PF	
XX	
XX	30-NOV-1981; 81JP-01933212.
PR	
XX	
PA	(TOXN) TOYO JOZO KK.
XX	
XX	
DR	WPI; 1983-709291/28.
XX	
PT	
XX	
PT	High activity human parathyroid hormone amide prodn. - by
PT	condensing protected aminoacid(s) and/or peptide(s) useful for
PT	lowering parathyroid gland function

XX Claim 1; Page 1; 20pp; Japanese.
 PS The human parathyroid hormone, hPTH(1-34)-amide was prep'd. by
 CC the following steps: Firstly the carboxy gp. at the C-terminal
 CC phenylalanine was converted into its amide form. The protected
 CC individual amino acids were condensed, in order, by liquid phase
 CC synthesis. The protecting groups were removed from the N-terminal
 CC amino gp. and other functional gps. by acidolysis, and the
 CC resulting hPTH(1-34)-amide purified by gel filtration
 CC chromatography using a Sephadex G-25, G-50 or LH-20 column or by
 CC column chromatography with carboxymethyl cellulose or ion exchange
 CC resin. The peptide amide is useful in lowering the activity of the
 CC parathyroid gland and in the prepn. of antibodies for diagnosis of
 CC parathyroid gland function.
 XX SQ Sequence 34 AA;
 Query Match 100.0%; Score 179; DB 4; Length 34;
 st Local Similarity 100.0%; Pred. No. 5,7e-16;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SVSEIQLMHNLGKHLNSMERVEWLKRLKLDVHNF 34
 DB 1 SVSEIQLMHNLGKHLNSMERVEWLKRLKLDVHNF 34
 RESULT 2
 AAP50377
 ID AAP50377 standard; peptide; 34 AA.
 XX AAP50377;
 AC AAP50377;
 XX 08-MAR-1992 (first entry)
 DT [Met(O)8,18]hPTH-(1-34).
 DE Human parathyroid hormone; calcium regulation.
 XX Homo sapiens.
 OS Key Location/Qualifiers
 FH Modified-site 8 /label= oxidised methionine
 FT Modified-site 18 /label= oxidised methionine
 FT Modified-site 18 /label= oxidised methionine
 XX JP59204159-A.
 PD 19-NOV-1984.
 XX 28-APR-1983; 83JP-0075607.
 PF 28-APR-1983; 83JP-0075607.
 PR (DAIL) DAICEL CHEM IND KK.
 XX WPI; 1985-003559/01.
 DR New (Met(O)8,18)hPTH-(1-34) peptide - increases calcium level in
 XX blood and decreases level in urine.
 PT Claim 1; Page 1; 3pp; Japanese.
 PS Unmodified hPTH(1-34) increases Ca in blood, decreases P in blood,
 CC decreases Ca in urine and increases P in urine by increasing cAMP in
 CC urine and enhancing vitamin D hydroxylase activity in kidneys. The
 CC modified derivative only has the effect of lowering Ca levels in
 CC urine and can be used when only this particular effect is required.
 XX SQ Sequence 34 AA;
 Query Match 100.0%; Score 179; DB 6; Length 34;

Best Local Similarity 100.0%; Pred. No. 5,7e-16;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SVSEIQLMHNLGKHLNSMERVEWLKRLKLDVHNF 34
 DB 1 SVSEIQLMHNLGKHLNSMERVEWLKRLKLDVHNF 34
 RESULT 3
 AAP60031
 ID AAP60031 standard; peptide; 34 AA.
 XX AAP60031;
 AC AAP60031;
 XX 06-JUL-1991 (first entry)
 DT Sequence of the first 34 AA residues of a parathyroid hormone
 DE obtainable from a human or animal.
 XX Osteoporosis therapy.
 OS Homo sapiens/animal.
 XX EP197514-A.
 FN 15-OCT-1986.
 PD 03-APR-1986; 86EP-0104562.
 PF 04-APR-1985; 85US-0720018.
 PR 05-DEC-1986; 86US-0939308.
 PR 21-MAY-1987; 87US-0052383.
 XX (GEHO-) GEN HOSPITAL CORP.
 FA Potts JT, Neer RM, Slovick DM;
 XX WPI; 1986-273437/42.
 DR Compn. and kits for increasing bone mass in osteoporosis -
 PT contg. parathyroid hormone or fragment with hydroxylated
 PT vitamin/D cpd. or calcium salt
 PS Claim 4; Page 24; 26pp; English.
 XX The peptide is used in a pharmaceutical compsn. together with a
 CC hydroxylated vitamin D compound, or a non-toxic calcium salt, pref.
 CC CaCO3. The compsn. pref. contains 100-700 (pref. 200-600, esp. 400-
 CC 500) units of the peptide. The vitamin D compound is pref. 1-alpha-
 CC hydroxy vitamin D2 or 1-alpha,25-dihydroxy vitamin D2.
 XX SQ Sequence 34 AA;
 Query Match 100.0%; Score 179; DB 7; Length 34;
 Best Local Similarity 100.0%; Pred. No. 5,7e-16;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SVSEIQLMHNLGKHLNSMERVEWLKRLKLDVHNF 34
 DB 1 SVSEIQLMHNLGKHLNSMERVEWLKRLKLDVHNF 34
 RESULT 4
 AAR07919
 ID AAR07919 standard; protein; 34 AA.
 XX AAR07919;
 AC AAR07919;
 XX 18-FEB-1991 (first entry)
 DT Human parathyroid hormone analogue, hPTH(7-34).
 DE Osteoporosis; hypercalcemia; hyperparathyroidism; hypertension.
 XX

XX OS Homo sapiens.
 XX PD US4968669-A.
 XX PD 06-NOV-1990.
 XX PF 21-APR-1989; 89US-0341597.
 XX PR 21-APR-1989; 89US-0341597.
 XX PR 09-MAY-1988; 88US-0191512.
 XX PA (MERI) MERCK & CO INC.
 XX PI Rosenblatt M, Chorev M;
 XX WPI; 1990-354642/47.
 XX
 PT New para:thyroid hormone analogues - which inhibit hormone
 PT activity by binding receptors while not producing second
 PT messenger molecules
 PT
 PS Claim 1; Column 8; 6pp; English.
 XX
 CC Peptide analogues have high affinity for PTH cell surface receptors,
 CC but do not stimulate production of secondary messenger molecules.
 CC They may be used in inhibition of PTH action, and in diagnosis and
 CC treatment of osteoporosis, hypercalcemia and hyperparathyroidism.
 CC Analogues may also be used in treatment of tumours and other cells
 CC overproducing peptide hormone-like substances, and immune diseases
 CC eg. allergic inflammation and hyperactive lymphocytes.
 CC Naturally occurring PTH levels may also be measured in vitro.
 XX
 SQ Sequence 34 AA;
 Query Match 100.0%; Score 179; DB 11; Length 34;
 Best Local Similarity 100.0%; Pred. No. 5.7e-16;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 SVSEIQLMHNGLKHLNSMERVEWLRKKLQDVHNF 34
 DB 1 SVSEIQLMHNGLKHLNSMERVEWLRKKLQDVHNF 34
 RESULT 5
 AAR22283
 ID AAR22283 standard; peptide; 34 AA.
 XX
 PS AAR22283;
 DT 29-JUL-1992 (first entry)
 XX
 DE Parathyroid hormone analogue N-terminus [1-34].
 KW Human; hPTH; wound healing; hair growth; hyperproliferation skin;
 KW disorders; psoriasis; cancer; burns.
 XX
 OS Homo sapiens.
 XX
 PN WO9204039-A.
 XX
 PD 19-MAR-1992.
 XX
 PF 30-AUG-1991; 91WO-US06218.
 XX
 PR 30-AUG-1990; 90US-0575219.
 XX
 PA (HOLI/) HOLICK M F.
 XX
 PI Hollick MF;
 XX
 WPI; 1992-114063/14.
 XX

PT Use of peptide having homology with parathyroid hormone - for
 PT enhancement of cell proliferation for wound healing
 XX
 PS Disclosure; Fig 1; 34pp; English.
 XX
 CC The peptide can be easily synthesised by recombinant DNA or solid
 CC phase peptide synthesis techniques. The peptide has > 50 percent
 CC homology with the N-terminal 1-34 amino acids of human parathyroid
 CC hormone or hypercalcaemic region. It is esp. PTH (7-34). The
 CC peptide may be used in a method for the treatment of hyperprolifer-
 CC ation skin disorders e.g. psoriasis, cancers, burns or skin
 CC ulcerations by inhibition of cell proliferation and enhancement of
 CC cell differentiation (agonist activity). They are also used to
 CC enhance cell proliferation (antagonist activity) for wound healing.
 CC They are also applicable in the promotion of new hair growth or
 CC stimulation of the rate of hair growth e.g. following chemotherapy
 CC or for treating alopecia e.g. male pattern baldness.
 XX
 SQ Sequence 34 AA;
 Query Match 100.0%; Score 179; DB 13; Length 34;
 Best Local Similarity 100.0%; Pred. No. 5.7e-16;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 SVSEIQLMHNGLKHLNSMERVEWLRKKLQDVHNF 34
 DB 1 SVSEIQLMHNGLKHLNSMERVEWLRKKLQDVHNF 34
 RESULT 6
 AAR41549
 ID AAR41549 standard; protein; 34 AA.
 XX
 AC AAR41549;
 XX
 DT 11-APR-1994 (first entry)
 XX
 DE [D-Ser3]hPTH (1-34)NH2.
 XX
 KW PTH; parathyroid hormone; protease resistance; osteoporosis;
 KW hypoparathyroidism; hypertension.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 3 /note = "D-form residue"
 FT Modified-site 34 /note = "C terminal is amidated"
 XX
 PN EP561412-A.
 XX
 PD 22-SEP-1993.
 XX
 PF 18-MAR-1993; 93EP-0104500.
 XX
 PR 19-MAR-1992; 92JP-0063517.
 XX
 PR 18-FEB-1993; 93JP-0029283.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Fukuda T, Nakagawa S, Taketomi S;
 XX
 DR WPI; 1993-296712/38.
 XX
 PT New parathyroid hormone deriva. - used for the treatment of
 PT osteoporosis hypoparathyroidism and hypertension
 XX
 PS Example 1; Page 17; 37pp; English.
 XX
 CC Human parathyroid hormone (PTH) analogues (AAR41548 - generic sequence;
 CC AAR41549-R41582 - specific examples) show increased resistance to
 CC proteases and a greater persistency of activity within the blood is

CC obtained. The proteins can be used to treat a number of bone and blood disorders. This analogue was used as a test compound.

XX Sequence 34 AA;

Query Match 100.0%; Score 179; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 5, 7e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLKRLKLDVHNF 34
Db 1 SVSEIQLMHNLGKHLNSMERVEWLKRLKLDVHNF 34

RESULT 7

AAR41570
ID AAR41570 standard; protein; 34 AA.

XX AAR41570;

b. 11-APR-1994 (first entry)

XX [Gln25]hPTH (1-34).

XX PTH; parathyroid hormone; protease resistance; osteoporosis;
KW hypoparathyroidism; hypertension.

XX Homo sapiens.

XX EP561412-A.

XX 22-SEP-1993.

XX 18-MAR-1993; 93EP-0104500.

XX 19-MAR-1992; 92JP-0063517.

XX 18-FEB-1993; 93JP-0029283.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Fukuda T, Nakagawa S, Taketomi S;

XX WPI; 1993-296712/38.

XX New parathyroid hormone derivs. - used for the treatment of
PT osteoporosis hypoparathyroidism and hypertension

XX Example 1; Page 27; 37pp; English.

CC Human parathyroid hormone (PTH) analogues (AAR41548 - generic sequence;
CC AAR41549-R41582 - specific examples) show increased resistance to
CC proteases and a greater persistency of activity within the blood is
CC obtained. The proteins can be used to treat a number of bone and blood
CC disorders. This analogue was used as a test compound.

XX Sequence 34 AA;

Query Match 100.0%; Score 179; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 5, 7e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLKRLKLDVHNF 34
Db 1 SVSEIQLMHNLGKHLNSMERVEWLKRLKLDVHNF 34

RESULT 8

AAR58291
ID AAR58291 standard; peptide; 34 AA.

XX AAR58291;

XX 20-SEP-1994 (first entry)

XX [Lys(For)26, Lys(For)27]-hPTH(1-34)-NH2.

XX Human parathyroid hormone; hPTH; variant; analogue;
KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
KW hypoparathyroidism.

XX Synthetic.

XX Key Location/Qualifiers
FH Modified-site 26 /label= Other
FT /note= "Formyl-Lys."
FT Modified-site 27 /label= Other
FT /note= "Formyl-Lys."
FT Modified-site 34 /note= "in amide form"

XX GB2269176-A.

XX 02-FEB-1994.

XX 12-JUL-1993; 93GB-0014384.

XX 15-JUL-1992; 92GB-0015009.

XX 18-DEC-1992; 92GB-0026415.

XX 23-DEC-1992; 92GB-0026859.

XX 23-DEC-1992; 92GB-0026861.

XX 28-JAN-1993; 93GB-0001691.

XX 28-JAN-1993; 93GB-0001692.

XX 14-APR-1993; 93GB-0007673.

XX 19-APR-1993; 93GB-0008033.

XX (SANO) SANDOZ LTD.

XX (BAUTE/) BAUER W.

XX (SANO) SANDOZ PATENT GMBH.

XX (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.

XX Albert R, Bauer W, Breckenridge R, Cardinaux F;

XX Gombert F, Gram H, Lewis I, Ramage P, Schneider H;

XX Waelchli R, Rainer A;

XX WPI; 1994-018352/03.

XX New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc.

XX Example 289; Page 47; 92pp; English.

XX This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.

XX Sequence 34 AA;

Query Match 100.0%; Score 179; DB 15; Length 34;
Best Local Similarity 100.0%; Pred. No. 5, 7e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLKRLKLDVHNF 34
Db 1 SVSEIQLMHNLGKHLNSMERVEWLKRLKLDVHNF 34

RESULT 9

AAR58228

ID AAR58228 standard; peptide; 34 AA.

XX

XX AAR58228;

XX

DT 20-SEP-1994 (first entry)
 XX [D-Asp30]-hPTH(1-34)-NH2.
 DE Human parathyroid hormone; hPTH; variant; analogue;
 KW Calcium; depletion; fixation; resorption; osteoporosis;
 KW hypoparathyroidism.
 XX Synthetic.
 OS
 FH Key Location/Qualifiers
 FT Misc-difference 30
 FT Modified-site /note= "D-form residue."
 FT 34
 FT Modified-site /note= "in amide form"
 FT 34
 XX
 PN GB2269176-A.
 XX
 PD 02-FEB-1994.
 XX
 PF 12-JUL-1993; 93GB-0014384.
 XX
 PR 15-JUL-1992; 92GB-0015009.
 PR 18-DEC-1992; 92GB-0026415.
 PR 23-DEC-1992; 92GB-0026859.
 PR 23-DEC-1992; 92GB-0026861.
 PR 28-JAN-1993; 93GB-0001691.
 PR 28-JAN-1993; 93GB-0001692.
 PR 28-JAN-1993; 93GB-0001692.
 PR 14-APR-1993; 93GB-0007673.
 PR 14-APR-1993; 93GB-0007673.
 PR 19-APR-1993; 93GB-0008033.
 XX
 PA (SANO) SANDOZ LTD.
 PA (BAUE/) BAUER W.
 PA (SANO) SANDOZ PATENT GMBH.
 PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
 XX
 PI Albert R, Bauer W, Breckenridge R, Cardinaux F;
 PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;
 PI Waelchli R, Rainer A;
 XX
 DR WPI; 1994-018352/03.
 XX
 PT New active para-thyroid hormone variants - used for treating or
 PT preventing osteoporosis etc.
 XX
 PS Example 226; Page 45; 92pp; English.
 XX
 CC This peptide is an example of a highly generic formula covering
 CC parathyroid hormone variants useful for treating or preventing bone
 CC conditions associated with calcium depletion/resorption, in cases
 CC where calcium fixation is required (esp. osteoporosis) or to treat
 CC hypoparathyroidism.
 XX
 SQ Sequence 34 AA;
 Query Match 100.0%; Score 179; DB 15; Length 34;
 Best Local Similarity 100.0%; Pred. No. 5.7e-16;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SVSEIQLMNLGKHLNSMERVWLKKLQDVHNF 34
 |||||
 Db 1 SVSEIQLMNLGKHLNSMERVWLKKLQDVHNF 34
 |||||
 RESULT 10
 AAR58016
 ID AAR58016 standard; peptide; 34 AA.
 XX
 AC AAR58016;
 XX
 DT 20-SEP-1994 (first entry)
 XX
 DE N-alpha-Isopropyl-hPTH(1-34)-NH2 parathyroid hormone variant.

XX Human parathyroid hormone; hPTH; variant; analogue;
 KW Calcium; depletion; fixation; resorption; osteoporosis;
 KW hypoparathyroidism.
 XX Synthetic.
 OS
 FH Key Location/Qualifiers
 FT Modified-site /note= "N-alpha-isopropyl-Ser"
 FT 34
 FT Modified-site /note= "in amide form"
 FT 34
 XX
 PN GB2269176-A.
 XX
 PD 02-FEB-1994.
 XX
 PF 12-JUL-1993; 93GB-0014384.
 XX
 PR 15-JUL-1992; 92GB-0015009.
 PR 18-DEC-1992; 92GB-0026415.
 PR 23-DEC-1992; 92GB-0026859.
 PR 23-DEC-1992; 92GB-0026861.
 PR 28-JAN-1993; 93GB-0001691.
 PR 28-JAN-1993; 93GB-0001692.
 PR 14-APR-1993; 93GB-0007673.
 PR 14-APR-1993; 93GB-0007673.
 PR 19-APR-1993; 93GB-0008033.
 XX
 PA (SANO) SANDOZ LTD.
 PA (BAUE/) BAUER W.
 PA (SANO) SANDOZ PATENT GMBH.
 PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
 XX
 PI Albert R, Bauer W, Breckenridge R, Cardinaux F;
 PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;
 PI Waelchli R, Rainer A;
 XX
 DR WPI; 1994-018352/03.
 XX
 PT New active para-thyroid hormone variants - used for treating or
 PT preventing osteoporosis etc.
 XX
 PS Example 1; Page 30; 92pp; English.
 XX
 CC This peptide is an example of a highly generic formula covering
 CC parathyroid hormone variants useful for treating or preventing bone
 CC conditions associated with calcium depletion/resorption, in cases
 CC where calcium fixation is required (esp. osteoporosis) or to treat
 CC hypoparathyroidism.
 XX
 SQ Sequence 34 AA;
 Query Match 100.0%; Score 179; DB 15; Length 34;
 Best Local Similarity 100.0%; Pred. No. 5.7e-16;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SVSEIQLMNLGKHLNSMERVWLKKLQDVHNF 34
 |||||
 Db 1 SVSEIQLMNLGKHLNSMERVWLKKLQDVHNF 34
 |||||
 RESULT 11
 AAR58017
 ID AAR58017 standard; peptide; 34 AA.
 XX
 AC AAR58017;
 XX
 DT 20-SEP-1994 (first entry)
 XX
 DE [Lys(N-epsilon-Isopropyl)26,27]-human parathyroid hormone (1-34)-NH2.
 XX
 KW Human parathyroid hormone; hPTH; variant; analogue;
 KW Calcium; depletion; fixation; resorption; osteoporosis;
 KW hypoparathyroidism.

XX hypoparathyroidism.
OS Synthetic.
XX Key Location/Qualifiers
FH Modified-site 26
FT Modified-site 27 /note= "N-epsilon-Iso-propyl-Lys"
FT Modified-site 27 /note= "N-epsilon-Iso-propyl-Lys"
FT Modified-site 34 /note= "in amide form"
XX
XX GB2269176-A.
XX
XX 02-FEB-1994.
XX
XX 12-JUL-1993; 93GB-0014384.
XX
XX 15-JUL-1992; 92GB-0015009.
XX 18-DEC-1992; 92GB-0026415.
XX 23-DEC-1992; 92GB-0026859.
XX 23-DEC-1992; 92GB-0026861.
XX 28-JAN-1993; 93GB-0001691.
XX 28-JAN-1993; 93GB-0001692.
XX 14-APR-1993; 93GB-0007673.
XX 19-APR-1993; 93GB-0008033.
XX (SANO) SANDOZ LTD.
PA (BAUE/) BAUER W.
PA (SANO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
XX
XX Albert R, Bauer W, Breckenridge R, Cardinaux P,
PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H,
PI Waelchli R, Rainer A,
XX WPI; 1994-018352/03.
XX
XX New active para-thyroid hormone variants - used for treating or
FT preventing osteoporosis etc.
XX
XX Example 2; Page 32; 92pp; English.
XX
XX This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.
SQ Sequence 34 AA;
Query Match 100.0%; Score 179; DB 15; Length 34;
Best Local Similarity 100.0%; Pred. No. 5,7e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SVSEIQLMHNLGKHLNSMERVEWLKRLQDVHNF 34
Db 1 SVSEIQLMHNLGKHLNSMERVEWLKRLQDVHNF 34
RESULT 12
AAR55724
ID AAR55724 standard; peptide; 34 AA.
XX
XX AAR55724;
XX
DT 16-NOV-1994 (first entry)
XX
XX Parathormone N-terminal sequence.
XX
XX Parathormone; parathyroid hormone; fatty acyl-peptide; conjugate;
KW antiproliferative; tumor; psoriasis; docosahexaenoic acid; EPA;
KW eicosapentaenoic acid; EPA; antitumor.

XX Synthetic.
OS WO9412530-A.
XX
XX 09-JUN-1994.
XX
XX 29-NOV-1993; 93WO-HU00065.
XX
XX 30-NOV-1992; 92US-0984293.
XX (BIOS-) BIOSIGNAL KUTATO FEJLESZTO KFT.
PA (SYNT-) SYNTHETIC PEPTIDES INC.
XX
XX Balogh A, Cachia PJ, Hodges RS, Horvath A, Keri G;
PI Szederkenyi F, Vadasz Z;
XX WPI; 1994-200194/24.
XX
XX New fatty acyl-peptide conjugates for inhibiting cell
PT proliferation - more active than free peptide, partic. for
PT treating tumours, virus-infected cells, psoriasis, etc.
XX
XX Disclosure; Fig. 1; 45pp; English.
XX
XX The peptides given in AAR55718-48 can each be conjugated through an
CC amide linkage with a polyunsaturated fatty acid moiety, such as
CC docosahexaenoic acid (DHA) or eicosapentaenoic acid, to improve
CC antiproliferative activity. The parathormone N-terminal fragment
CC inhibits osteoblast proliferation.
XX
SQ Sequence 34 AA;
Query Match 100.0%; Score 179; DB 15; Length 34;
Best Local Similarity 100.0%; Pred. No. 5,7e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SVSEIQLMHNLGKHLNSMERVEWLKRLQDVHNF 34
Db 1 SVSEIQLMHNLGKHLNSMERVEWLKRLQDVHNF 34
RESULT 13
AAR74521
ID AAR74521 standard; Peptide; 34 AA.
XX
XX AAR74521;
XX
XX 04-DEC-1995 (first entry)
XX
XX Human parathyroid hormone (1-34).
XX
XX Analogue; truncated human parathyroid hormone; PTH; hPTH; substitution;
KW osteoporosis; hypercalcaemia; hyperparathyroidism;
KW metabolic bone disease; human; veterinary medicine;
KW iontophoretic transdermal transport; recombinant E.coli.
XX
XX Homo sapiens.
XX
XX WO9511988-A.
XX
XX 04-MAY-1995.
XX
XX 25-OCT-1994; 94WO-US12205.
XX
XX 25-OCT-1993; 93US-0142551.
XX (APFY-) APFYMAX TECHNOLOGIES NV.
XX
XX Oldenburg KR, Selick HE;
XX WPI; 1995-178880/23.
XX

PT New active analogues of parathyroid hormone - with increased
PT activity, stability in serum etc., esp. for treating
PT osteoporosis, also related DNA and vectors
XX Disclosure; Page 1; 109pp; English.
XX This sequence represents residues 1-34 of human parathyroid hormone
CC (RPTH). This sequence was used in the production of analogues of the
CC truncated form of PTH. These analogues have increased activity and
CC longer serum half life than native PTH due to eg. substitution of Met
CC residues with Leu residues and replacing the carboxy Phe with Tyr. The
CC carboxy terminal may also be modified by the addition of a homoserine
CC residue or analogue, or by the addition of residues 35-84 of wild type
CC PTH (see AAR74410). These PTH analogues may be used in the treatment of
CC osteoporosis or hypercalcaemia, hyperparathyroidism or other metabolic
CC bone diseases in human or veterinary medicine. These peptides may also
CC have increased iontophoretic transdermal transport compared to wild type
CC PTH and can be produced in high yield in recombinant E.coli.
XX Sequence 34 AA;
SQ
Query Match 100.0%; Score 179; DB 16; Length 34;
Best Local Similarity 100.0%; Pred. No. 5.7e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SVSEIQLMNLGKHLNSMERVEWLKRLQDVHNF 34
DB 1 SVSEIQLMNLGKHLNSMERVEWLKRLQDVHNF 34
RESULT 14
AAW99449
ID AAW99449 standard; peptide; 34 AA.
XX AAW99449;
XX 08-JUN-1999 (first entry)
XX Human parathyroid hormone aal-34.
XX Parathyroid hormone; PTH; parathormone; premature birth; pregnancy;
KW spontaneous abortion; uterine contraction; human.
XX Homo sapiens.
XX US5880093-A.
XX 09-MAR-1999.
XX 05-APR-1995; 95US-0411726.
XX 28-SEP-1992; 92IT-MI02331.
XX (BAGN/) BAGNOLI F.
XX Bagnoli F;
XX WPI; 1996-162392/17.
XX Use of composition containing parathormone or fragments - for
PT preventing premature birth or spontaneous abortion or for treating
PT unwanted uterine contractions
XX Disclosure; Column 7-8; 11pp; English.
XX Peptides AAW99448-W99452 represent all or part of the parathyroid
CC hormone (PTH; parathormone) sequence or related peptide. The peptides
CC are used for preventing premature birth, spontaneous abortion or unwanted
CC uterine contractions in a pregnant human patient.
CC (Note: this patent is the first Major Country Equivalent to Italian
CC Patent IT1255388).
XX Sequence 34 AA;
SQ

Query Match 100.0%; Score 179; DB 17; Length 34;
Best Local Similarity 100.0%; Pred. No. 5.7e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SVSEIQLMNLGKHLNSMERVEWLKRLQDVHNF 34
DB 1 SVSEIQLMNLGKHLNSMERVEWLKRLQDVHNF 34
RESULT 15
AAR99978
ID AAR99978 standard; peptide; 34 AA.
XX AAR99978;
XX 30-APR-1997 (first entry)
XX Human parathyroid hormone peptide fragment (1-34).
XX cyclic parathyroid hormone fragment; calcium-regulating activity;
KW osteoporosis; inhibit proliferation; epidermal cell; psoriasis;
KW improved half life; calcium retention; bone.
XX Synthetic.
XX DE19508672-A1.
XX 12-SEP-1996.
XX 10-MAR-1995; 95DE-1008672.
XX 10-MAR-1995; 95DE-1008672.
XX (BOEF) BOEHRINGER MANNHEIM GMBH.
XX Dony C, Esswein A, Hoffmann E, Honold K, Schaefer W;
XX WPI; 1996-413519/42.
XX Cyclic parathyroid hormone fragments with lactam bridge - have good
PT in vivo half life and are useful for treating osteoporosis and
PT preventing epidermal cell proliferation
XX Disclosure; Page 9; 14pp; German.
XX New cyclic parathyroid hormone fragments (CPTH) have the amino acid
CC sequence of h, b, p, r or CPTH(1-34), opt. extended by up to 4 amino
CC acids (aa) at the C-terminus and opt. shortened by up to 3 amino acids at
CC the N-terminus, and are cyclised between positions 13 and 17. One of
CC these positions is occupied by L- or D- Orn or Lys, and the other by L-
CC or D- Glu or Asp. CPTH have calcium-regulating activity (esp. for
CC treating osteoporosis and inhibit proliferation of epidermal cells (for
CC treating psoriasis). The CPTH have an improved half life in vivo than
CC known PTH fragments, increased mitogenicity and DNA-synthesising
CC capacity, reduced catabolic, calcium-mobilising activity and increased
CC activity for calcium retention and incorporation into bone. The
CC present sequence is that of human PTH peptide fragment (1-34).
XX Sequence 34 AA;
SQ
Query Match 100.0%; Score 179; DB 17; Length 34;
Best Local Similarity 100.0%; Pred. No. 5.7e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SVSEIQLMNLGKHLNSMERVEWLKRLQDVHNF 34
DB 1 SVSEIQLMNLGKHLNSMERVEWLKRLQDVHNF 34
Search completed: April 9, 2003, 16:44:14
Job time : 37 secs

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OM protein - protein search, using sw model

Run on: April 9, 2003, 16:43:37 ; Search time 15 Seconds
(without alignments)
66.692 Million call updates/sec

Title: us-09-843-221a-16

Perfect score: 179.000000
Sequence: 1 SVSEIQLMNLGKHLNMRVWLKQLQDVHNF 34

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

number of hits satisfying chosen parameters: 189198

Minimum DB seq length: 0
Maximum DB seq length: 70

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: 1 Issued Patents-AA:
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3: /cgn2_6/prodata/1/iaa/5B COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6A COMB.pep.*
5: /cgn2_6/prodata/1/iaa/6B COMB.pep.*
6: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep.*
7: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	179	100.0	34	1 US-07-765-373-1	Sequence 1, Appli
2	179	100.0	34	1 US-08-033-099-1	Sequence 1, Appli
3	179	100.0	34	1 US-08-262-495C-1	Sequence 1, Appli
4	179	100.0	34	1 US-07-915-247A-1	Sequence 1, Appli
5	179	100.0	34	1 US-08-443-863-1	Sequence 1, Appli
6	179	100.0	34	1 US-08-448-070-1	Sequence 1, Appli
7	179	100.0	34	1 US-08-488-105-7	Sequence 1, Appli
8	179	100.0	34	1 US-08-468-275-6	Sequence 6, Appli
9	179	100.0	34	1 US-08-449-500-1	Sequence 1, Appli
10	179	100.0	34	1 US-08-449-317A-1	Sequence 1, Appli
11	179	100.0	34	2 US-08-142-551B-2	Sequence 2, Appli
12	179	100.0	34	2 US-08-477-022-1	Sequence 1, Appli
13	179	100.0	34	2 US-08-449-447-1	Sequence 1, Appli
14	179	100.0	34	2 US-08-835-231-13	Sequence 13, Appli
15	179	100.0	34	2 US-08-184-328-1	Sequence 1, Appli
16	179	100.0	34	2 US-08-411-726-2	Sequence 2, Appli
17	179	100.0	34	2 US-08-691-647C-5	Sequence 5, Appli
18	179	100.0	34	2 US-08-521-097-1	Sequence 1, Appli
19	179	100.0	34	3 US-09-044-536A-1	Sequence 1, Appli
20	179	100.0	34	3 US-08-904-760B-22	Sequence 22, Appli
21	179	100.0	34	4 US-09-108-661-13	Sequence 13, Appli
22	179	100.0	34	4 US-09-007-466-6	Sequence 6, Appli
23	179	100.0	34	4 US-09-406-813-1	Sequence 1, Appli
24	179	100.0	34	4 US-08-952-980B-6	Sequence 6, Appli
25	179	100.0	34	5 PCT-US95-15800-22	Sequence 22, Appli
26	179	100.0	35	1 US-08-256-363-3	Sequence 3, Appli
27	179	100.0	36	1 US-08-256-363-4	Sequence 4, Appli

28	179	100.0	37	1 US-08-440-117-1	Sequence 1, Appli
29	179	100.0	37	4 US-09-068-738A-16	Sequence 16, Appli
30	179	100.0	38	1 US-08-112-024-1	Sequence 1, Appli
31	179	100.0	38	1 US-08-232-849-1	Sequence 1, Appli
32	179	100.0	38	2 US-08-625-586-1	Sequence 1, Appli
33	179	100.0	38	3 US-09-128-401-1	Sequence 1, Appli
34	176	98.3	34	4 US-08-903-497A-1	Sequence 1, Appli
35	176	98.3	34	4 US-09-635-076-1	Sequence 1, Appli
36	175	97.8	34	1 US-08-488-105-1	Sequence 1, Appli
37	175	97.8	34	1 US-08-488-105-13	Sequence 13, Appli
38	175	97.8	36	1 US-08-112-024-2	Sequence 2, Appli
39	174	97.2	34	3 US-09-044-536A-9	Sequence 9, Appli
40	173	96.6	34	3 US-09-044-536A-10	Sequence 10, Appli
41	173	96.6	34	3 US-08-904-760B-9	Sequence 9, Appli
42	172	96.1	34	1 US-08-262-495C-2	Sequence 2, Appli
43	172	96.1	34	3 US-09-044-536A-13	Sequence 13, Appli
44	172	96.1	34	3 US-09-044-536A-14	Sequence 14, Appli
45	172	96.1	34	3 US-09-044-536A-15	Sequence 15, Appli

ALIGNMENTS

RESULT 1
US-07-765-373-1
Sequence 1, Application US/07765373
Patent No. 5393862
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, Shizue
APPLICANT: FUKUDA, Teunehiko
APPLICANT: KAWASE, Masahiro
APPLICANT: YAMAZAKI, Iwao
TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESS: CUSHMAN
STREET: 130 Water Street
CITY: Boston
STATE: Massachusetts
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/765,373
FILING DATE: 19910925
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, Gregory D.
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: 41289
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 20991 STRE UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
US-07-765-373-1

Query Match 100.0%; Score 179; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.8e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SVSEIQLMNLGKHLNMRVWLKQLQDVHNF 34

Db 1 SVSEIQLMHNLGKHLNSMVERVWLKRLQDVHNF 34

RESULT 2

US-08-033-099-1

Sequence 1, Application US/08033099

Patent No. 5434246

GENERAL INFORMATION:

APPLICANT: FUKUDA, Tsunehiko

APPLICANT: NAKAGAWA, Shizue

APPLICANT: TAKETOMI, Shigehisa

TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &

ADDRESSEE: CUSHMAN

STREET: 130 Water Street

CITY: Boston

STATE: Massachusetts

COUNTRY: US

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/033,099

FILING DATE: 19930316

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: WILLIAMS, Gregory D

REGISTRATION NUMBER: 30901

REFERENCE/DOCKET NUMBER: 42528

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)523-3400

TELEFAX: (613)523-6440

TELEX: 200291 STRE UR

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 34 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: N-terminal

US-08-033-099-1

Query Match 100.0%; Score 179; DB 1; Length 34;

Best Local Similarity 100.0%; Pred. No. 3.8e-17;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMVERVWLKRLQDVHNF 34

Db 1 SVSEIQLMHNLGKHLNSMVERVWLKRLQDVHNF 34

RESULT 3

US-08-262-495C-1

Sequence 1, Application US/08262495C

Patent No. 5556940

GENERAL INFORMATION:

APPLICANT: WILLICK, Gordon E.

APPLICANT: WHITFIELD, James F.

APPLICANT: SUREWICZ, Witold

APPLICANT: SUNG, Wing L.

APPLICANT: NEUGENBAUER, Witold

TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kirby, Eades, Gale, Baker

STREET: 112 Kent Street, Suite 770,

CITY: Ottawa
COUNTRY: Canada
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/262,495C
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: EADES, No. 5556940ris M.
REGISTRATION NUMBER: 5,263
REFERENCE/DOCKET NUMBER: 36210
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613)-237-6900
TELEFAX: (613)-237-0045

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 34 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-262-495C-1

Query Match 100.0%; Score 179; DB 1; Length 34;

Best Local Similarity 100.0%; Pred. No. 3.8e-17;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMVERVWLKRLQDVHNF 34

Db 1 SVSEIQLMHNLGKHLNSMVERVWLKRLQDVHNF 34

RESULT 4

US-07-915-247A-1

Sequence 1, Application US/07915247A

Patent No. 5589452

GENERAL INFORMATION:

APPLICANT: Krstenansky, John L.

APPLICANT: Nestor Jr., John J.

APPLICANT: Ho, Teresa H.

APPLICANT: Vickery, Brian H.

APPLICANT: Bach, Chinh T.

TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND

TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:

ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.

STREET: 3401 Hillview Ave.

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/915,247A

FILING DATE: 19920714

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Schmonsees, William

REGISTRATION NUMBER: 31,796

REFERENCE/DOCKET NUMBER: 27610

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-6593
TELEFAX: 415-496-3529
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
US-07-915-247A-1

Query Match 100.0%; Score 179; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.8e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMNHLGKHLNSMERVWLKQLQDVHNF 34
|||||
DB 1 SVSEIQLMNHLGKHLNSMERVWLKQLQDVHNF 34
|||||

RESULT 5
US-08-443-863-1
Sequence 1, Application US/08443863
Patent No. 5693616
GENERAL INFORMATION:
APPLICANT: Kristenansky, John L.
APPLICANT: Nestor Jr., John J.
APPLICANT: Ho, Teresa H.
APPLICANT: Vickery, Brian H.
APPLICANT: Bach, Chinh T.

TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND
TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
STREET: 3401 Hillview Ave.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94303

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,863
FILING DATE: 14-JUL-1992
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: Schmonsees, William
REGISTRATION NUMBER: 31,796
REFERENCE/DOCKET NUMBER: 27610
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-6593
TELEFAX: 415-496-3529
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
US-08-443-863-1

Query Match 100.0%; Score 179; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.8e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMNHLGKHLNSMERVWLKQLQDVHNF 34
|||||
DB 1 SVSEIQLMNHLGKHLNSMERVWLKQLQDVHNF 34
|||||

US-08-443-863-1
Sequence 1, Application US/08443863
Patent No. 5693616
GENERAL INFORMATION:
APPLICANT: Kristenansky, John L.
APPLICANT: Nestor Jr., John J.
APPLICANT: Ho, Teresa H.
APPLICANT: Vickery, Brian H.
APPLICANT: Bach, Chinh T.

TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND
TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
STREET: 3401 Hillview Ave.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94303

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,863
FILING DATE: 14-JUL-1992
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: Schmonsees, William
REGISTRATION NUMBER: 31,796
REFERENCE/DOCKET NUMBER: 27610
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-6593
TELEFAX: 415-496-3529
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
US-08-443-863-1

QY 1 SVSEIQLMNHLGKHLNSMERVWLKQLQDVHNF 34
|||||
DB 1 SVSEIQLMNHLGKHLNSMERVWLKQLQDVHNF 34
|||||

RESULT 6

US-08-448-070-1
Sequence 1, Application US/08448070
Patent No. 5695955
GENERAL INFORMATION:
APPLICANT: Kristenansky, John L.
APPLICANT: Nestor Jr., John J.
APPLICANT: Ho, Teresa H.
APPLICANT: Vickery, Brian H.
APPLICANT: Bach, Chinh T.

TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND
TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
STREET: 3401 Hillview Ave.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94303

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,070
FILING DATE: 14-JUL-1992
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Schmonsees, William
REGISTRATION NUMBER: 31,796
REFERENCE/DOCKET NUMBER: 27610
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-6593
TELEFAX: 415-496-3529
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
US-08-448-070-1

Query Match 100.0%; Score 179; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.8e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMNHLGKHLNSMERVWLKQLQDVHNF 34
|||||
DB 1 SVSEIQLMNHLGKHLNSMERVWLKQLQDVHNF 34
|||||

RESULT 7

US-08-488-105-7
Sequence 7, Application US/08488105
Patent No. 5717062
GENERAL INFORMATION:
APPLICANT: Choev, Michael
APPLICANT: Rosenblatt, Michael
TITLE OF INVENTION: CYCLIC ANALOGS OF PTH AND PTHrP
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street

TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND
TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
STREET: 3401 Hillview Ave.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94303

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,070
FILING DATE: 14-JUL-1992
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Schmonsees, William
REGISTRATION NUMBER: 31,796
REFERENCE/DOCKET NUMBER: 27610
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-6593
TELEFAX: 415-496-3529
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
US-08-448-070-1

Query Match 100.0%; Score 179; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.8e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMNHLGKHLNSMERVWLKQLQDVHNF 34
|||||
DB 1 SVSEIQLMNHLGKHLNSMERVWLKQLQDVHNF 34
|||||

CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,105
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Tsao, Y. Rocky
REGISTRATION NUMBER: 34,053
REFERENCE/DOCKET NUMBER: 00537/112001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
OTHER INFORMATION: The side chains of Lys at position 26 and Asp at position 30 are linked by an amide bond and this sequence has an amide C-terminus (i.e., CONH2), rather than a carboxy C-terminus (i.e., COOH).
US-08-488-105-7

Query Match 100.0%; Score 179; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.8e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNGLGKHLNSMERVWLKRLKQDVHNF 34
Db 1 SVSEIQLMHNGLGKHLNSMERVWLKRLKQDVHNF 34

RESULT 8
US-08-468-275-6
Sequence 6, Application US/08468275
Patent No. 5747453
GENERAL INFORMATION:
APPLICANT: HOLLADAY, LESLIE A.
APPLICANT: OLDENBURG, KEVIN R.
TITLE OF INVENTION: METHOD FOR INCREASING THE
TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALZA CORPORATION
STREET: 950 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94303-0802
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,275
FILING DATE: 06-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MILLER, D. BYRON
REGISTRATION NUMBER: 30,661

REFERENCE/DOCKET NUMBER: 0360-0002; ARC-2349
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 496-8150
TELEFAX: (415) 496-8048
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-468-275-6

Query Match 100.0%; Score 179; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.8e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNGLGKHLNSMERVWLKRLKQDVHNF 34
Db 1 SVSEIQLMHNGLGKHLNSMERVWLKRLKQDVHNF 34

RESULT 9
US-08-449-500-1
Sequence 1, Application US/08449500
Patent No. 5798225
GENERAL INFORMATION:
APPLICANT: Krstenansky, John L.
APPLICANT: Nestor Jr., John J.
APPLICANT: Ho, Teresa H.
APPLICANT: Vickery, Brian H.
APPLICANT: Bach, Chinh T.
TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND
TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE
FOR THE TREATMENT OF OSTEOPOROSIS
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
STREET: 3401 Hillview Ave.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94303

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,500
FILING DATE: 18-JAN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Schmonsees, William
REGISTRATION NUMBER: 31,796
REFERENCE/DOCKET NUMBER: 27610-P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-6593
TELEFAX: 415-496-3529
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
US-08-449-500-1

Query Match 100.0%; Score 179; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.8e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMNLGKHLNSMERVWLKRLQDVHNF 34
 DB 1 SVSEIQLMNLGKHLNSMERVWLKRLQDVHNF 34

RESULT 10

US-08-449-317A-1
 ; Sequence 1, Application US/08449317A
 ; Patent No. 5807823
 ; GENERAL INFORMATION:
 ; APPLICANT: Vickery, Brian H.
 ; TITLE OF INVENTION: METHOD FOR TREATMENT OF CORTICOSTEROID
 ; TITLE OF INVENTION: INDUCED OSTEOPENIA
 ; NUMBER OF SEQUENCES: 86
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
 ; STREET: 3401 Hillview Ave.
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94303

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/449,317A
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Schmonsees, William
 REGISTRATION NUMBER: 31,796
 REFERENCE/DOCKET NUMBER: 27610-P2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-6593
 TELEFAX: 415-496-3529
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 34 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHEICAL: NO
 FRAGMENT TYPE: N-terminal
 US-08-449-317A-1

Query Match 100.0%; Score 179; DB 1; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.8e-17; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMNLGKHLNSMERVWLKRLQDVHNF 34
 DB 1 SVSEIQLMNLGKHLNSMERVWLKRLQDVHNF 34

RESULT 11

US-08-142-551B-2
 ; Sequence 2, Application US/08142551B
 ; Patent No. 5814603
 ; GENERAL INFORMATION:
 ; APPLICANT: Oldenburg, Kevin R.
 ; APPLICANT: Selick, Harold E.
 ; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
 ; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
 ; NUMBER OF SEQUENCES: 132
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Burns, Doane, Swecker & Mathis
 ; STREET: 699 Prince Street
 ; CITY: Alexandria
 ; STATE: Virginia
 ; COUNTRY: US
 ; ZIP: 22313

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/142,551B
 FILING DATE: 25-OCT-1993
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/077,296
 FILING DATE: 14-JUN-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/898,219
 FILING DATE: 12-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/965,677
 FILING DATE: 22-OCT-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Swiss, Gerald F.
 REGISTRATION NUMBER: 30,113
 REFERENCE/DOCKET NUMBER: 000324-010
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 854-7400
 TELEFAX: (415) 854-8275
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 34 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Peptide
 LOCATION: 1..34
 OTHER INFORMATION: /note= "The sequence of the 34
 amino acid truncated human PTH peptide,
 OTHER INFORMATION: designated: Human PTH."
 US-08-142-551B-2

Query Match 100.0%; Score 179; DB 2; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.8e-17; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMNLGKHLNSMERVWLKRLQDVHNF 34
 DB 1 SVSEIQLMNLGKHLNSMERVWLKRLQDVHNF 34

RESULT 12

US-08-477-022-1
 ; Sequence 1, Application US/08477022
 ; Patent No. 5821225
 ; GENERAL INFORMATION:
 ; APPLICANT: Vickery, Brian H.
 ; TITLE OF INVENTION: METHOD FOR TREATMENT OF CORTICOSTEROID
 ; TITLE OF INVENTION: INDUCED OSTEOPENIA
 ; NUMBER OF SEQUENCES: 86
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
 ; STREET: 3401 Hillview Ave.
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94303
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/477,022
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Schmonsees, William
REGISTRATION NUMBER: 31,796
REFERENCE/DOCKET NUMBER: 27610-P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-955-6593
TELEFAX: 415-496-3529
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
US-08-477-022-1

Query Match	100.0%	Score 179;	DB 2;	Length 34;
Best Local Similarity	100.0%	Pred. No. 3.8e-17;		
atches 34; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

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Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 13
 US-08-449-447-1
 ; Sequence 1, Application US/08449447
 ; Patent No. 5840837
 ; GENERAL INFORMATION:
 ; APPLICANT: Krestenansky, John L.
 ; APPLICANT: Nestor Jr., John J.
 ; APPLICANT: Ho, Teresa H.
 ; APPLICANT: Vickery, Brian H.
 ; APPLICANT: Bach, Chinh T.
 ; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND
 ; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE
 ; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
 ; NUMBER OF SEQUENCES: 86
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
 ; STREET: 3401 Hillview Ave.
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94303

Query Match: 100.0%; Score 179; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.8e-17;
Matches 34; Conservative 0; Mismatches 0; Indels

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|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKQLQDVHNF 34

RESULT 14
US-08-835-231-13
; Sequence 13, Application US/08835231
; Patent No. 5861284
; GENERAL INFORMATION:
; APPLICANT: NISHIMURA, Osamu
; APPLICANT: KURIYAMA, Masato
; APPLICANT: KOYAMA, NO. 5861284nyuki
; APPLICANT: FUKUDA, Tsunehiko
; TITLE OF INVENTION: METHOD FOR PRODUCING A BIOLOGICALLY
; TITLE OF INVENTION: ACTIVE RECOMBINANT CYSTEINE-FREE
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:

Query Match	100.0%;	Score 179;	DB 2;	Length 34;
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Db 1 SVSEIQLMHNLGKHLNSMERVWLRRKKLQDVHNF 34
RESULT 15
US-08-184-328-1
; Sequence 1, Application US/08184328
; Patent No. 5874086
; GENERAL INFORMATION:
; APPLICANT: Krstenansky, John L.
; APPLICANT: Nestor Jr., John J.
; APPLICANT: Ho, Teresa H.
; APPLICANT: Vickery, Brian H.
; APPLICANT: Bach, Chinh T.
; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND
; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
; STREET: 3401 Hillview Ave.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/184,328
; FILING DATE: 18-JAN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Schmonsees, William
; REGISTRATION NUMBER: 31,796
; REFERENCE/DOCKET NUMBER: 27610-P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-6593
; TELEFAX: 415-496-3529
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; FRAGMENT TYPE: N-terminal
; US-08-184-328-1
Query Match 100.0%; Score 179; DB 2; Length 34;
Best Local Similarity 100.0%; Fred. No. 3.8e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SVSEIQLMHNLGKHLNSMERVWLRRKKLQDVHNF 34
Db 1 SVSEIQLMHNLGKHLNSMERVWLRRKKLQDVHNF 34

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Search completed: April 9, 2003, 16:45:51
Job time : 16 secs

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